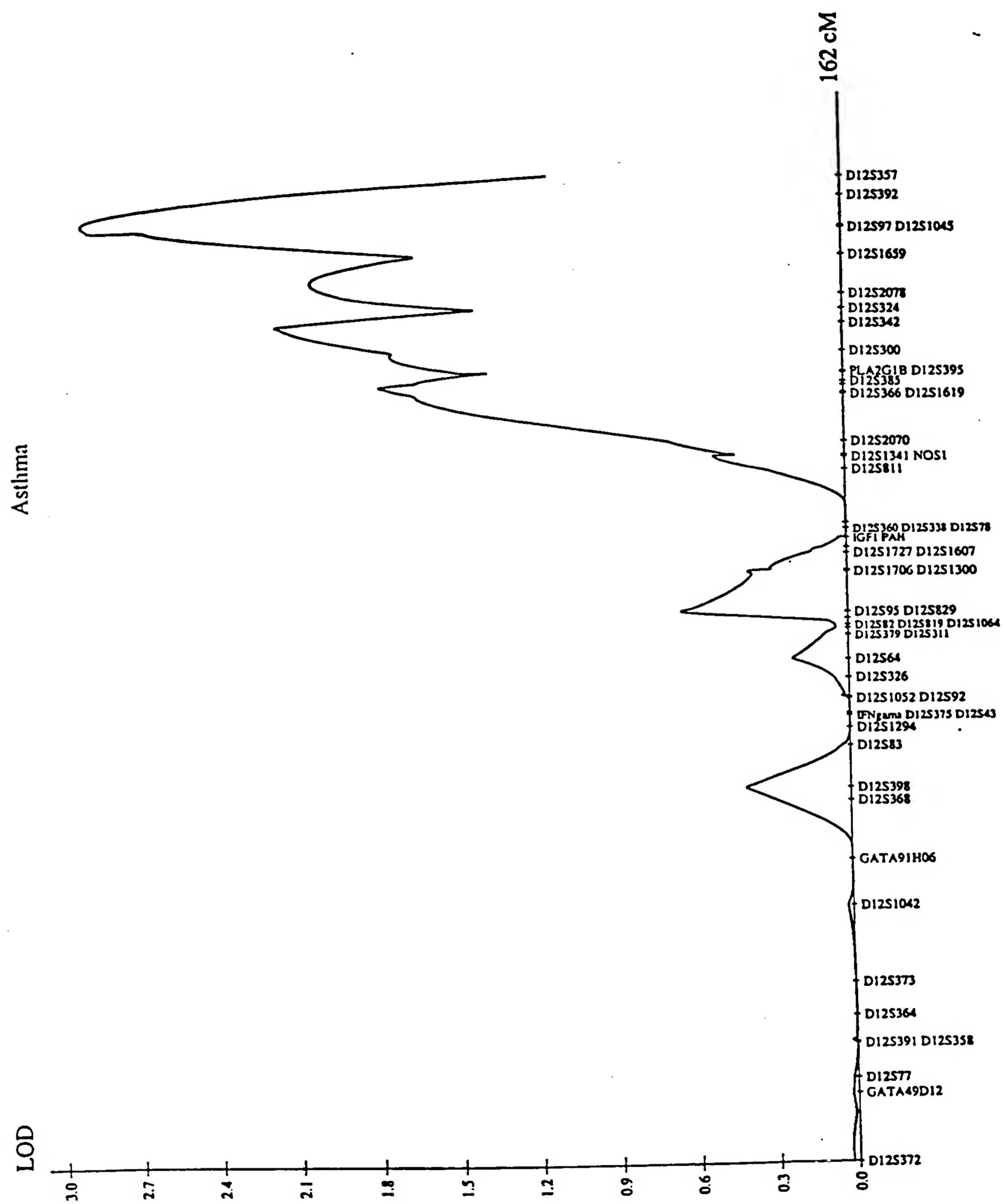
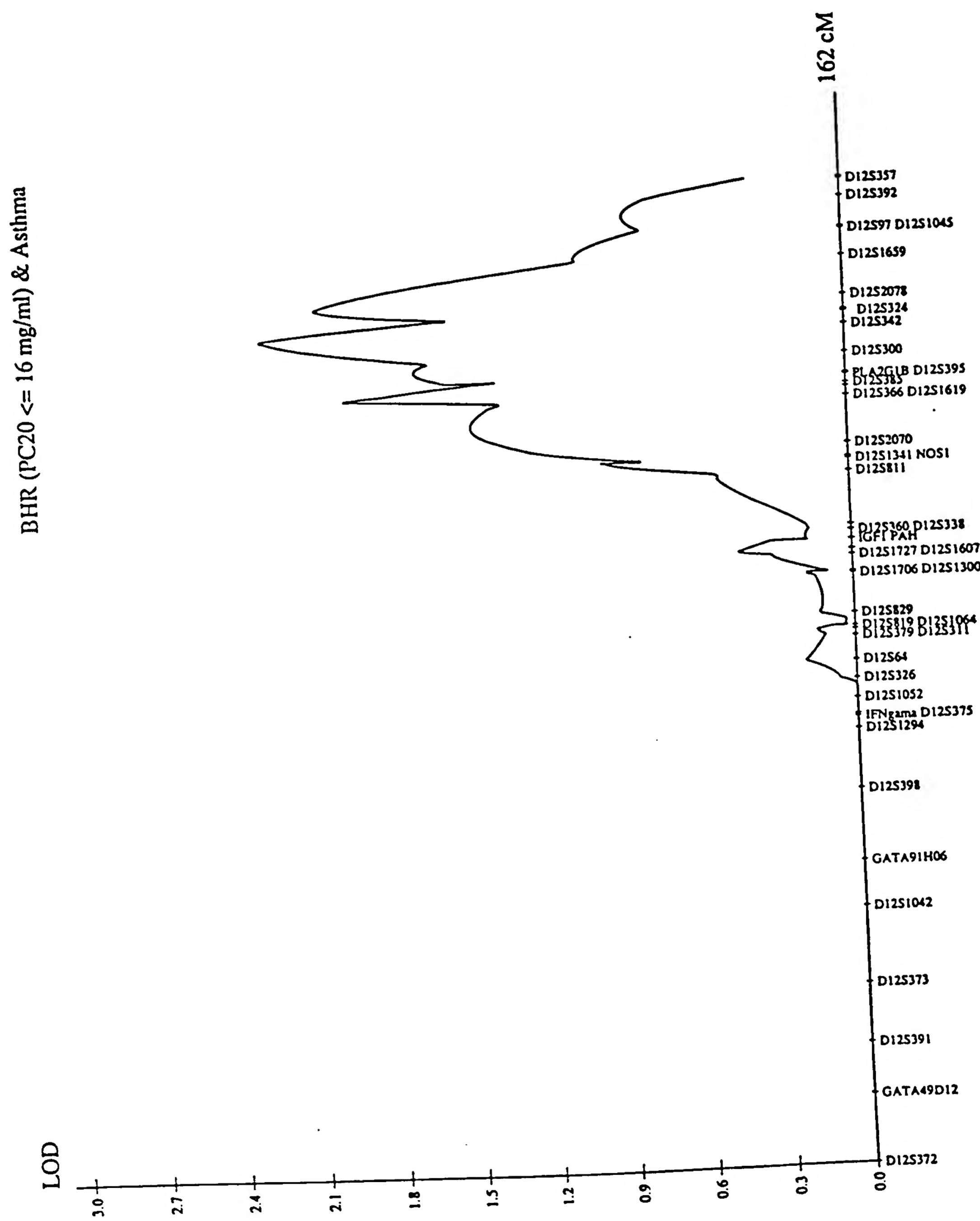


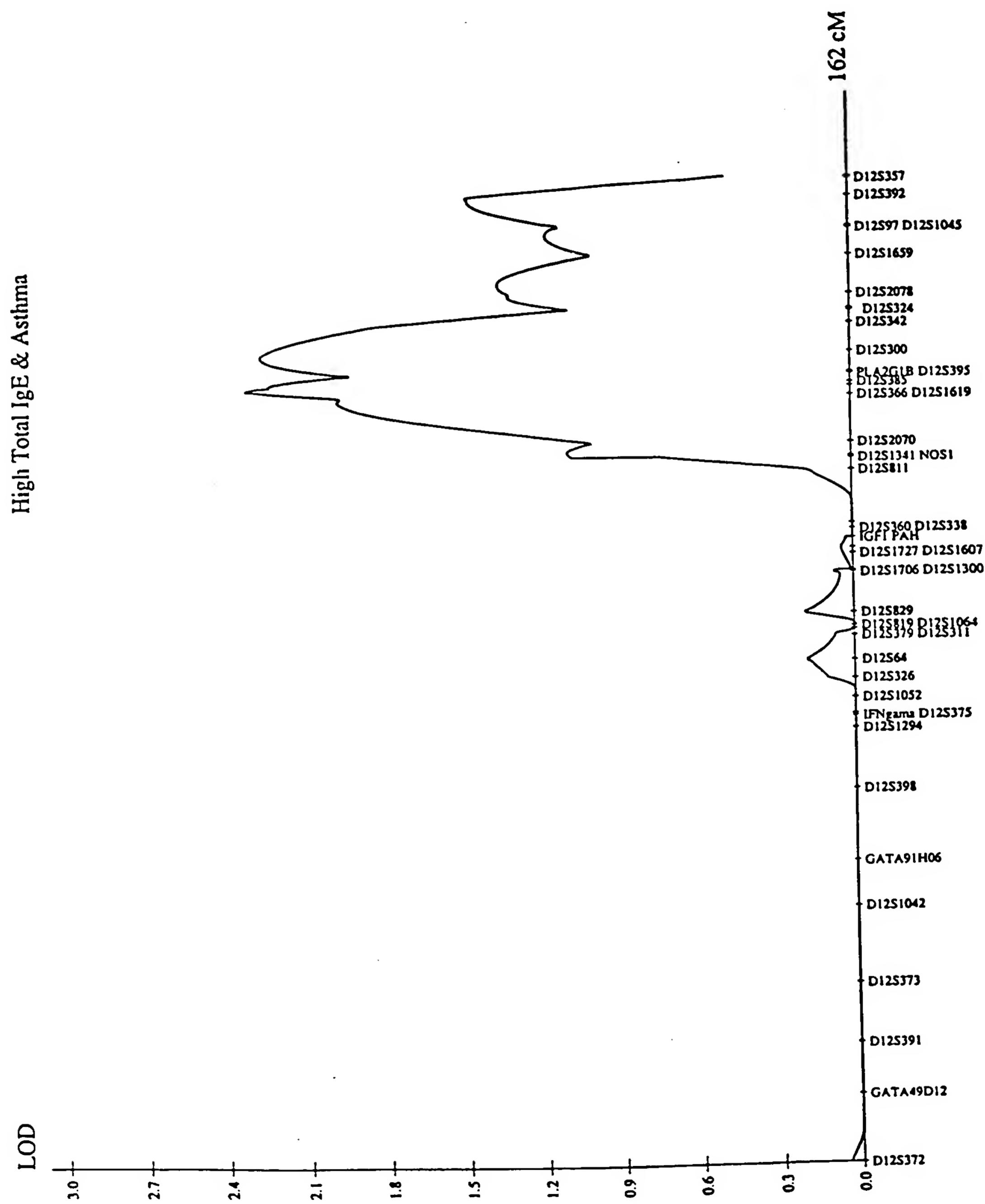
**FIG. 1A**



**FIG. 1B**

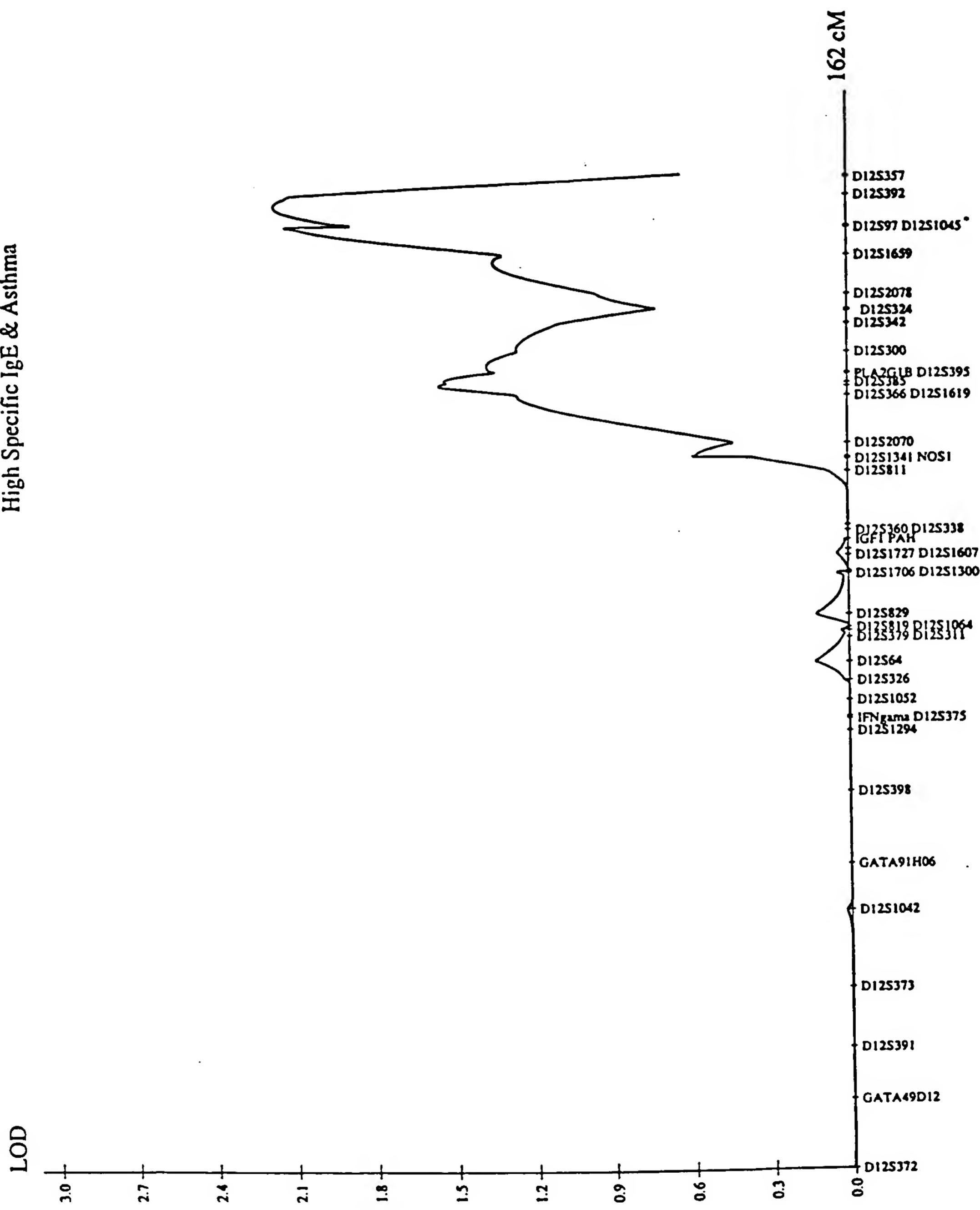


**FIG. 1C**

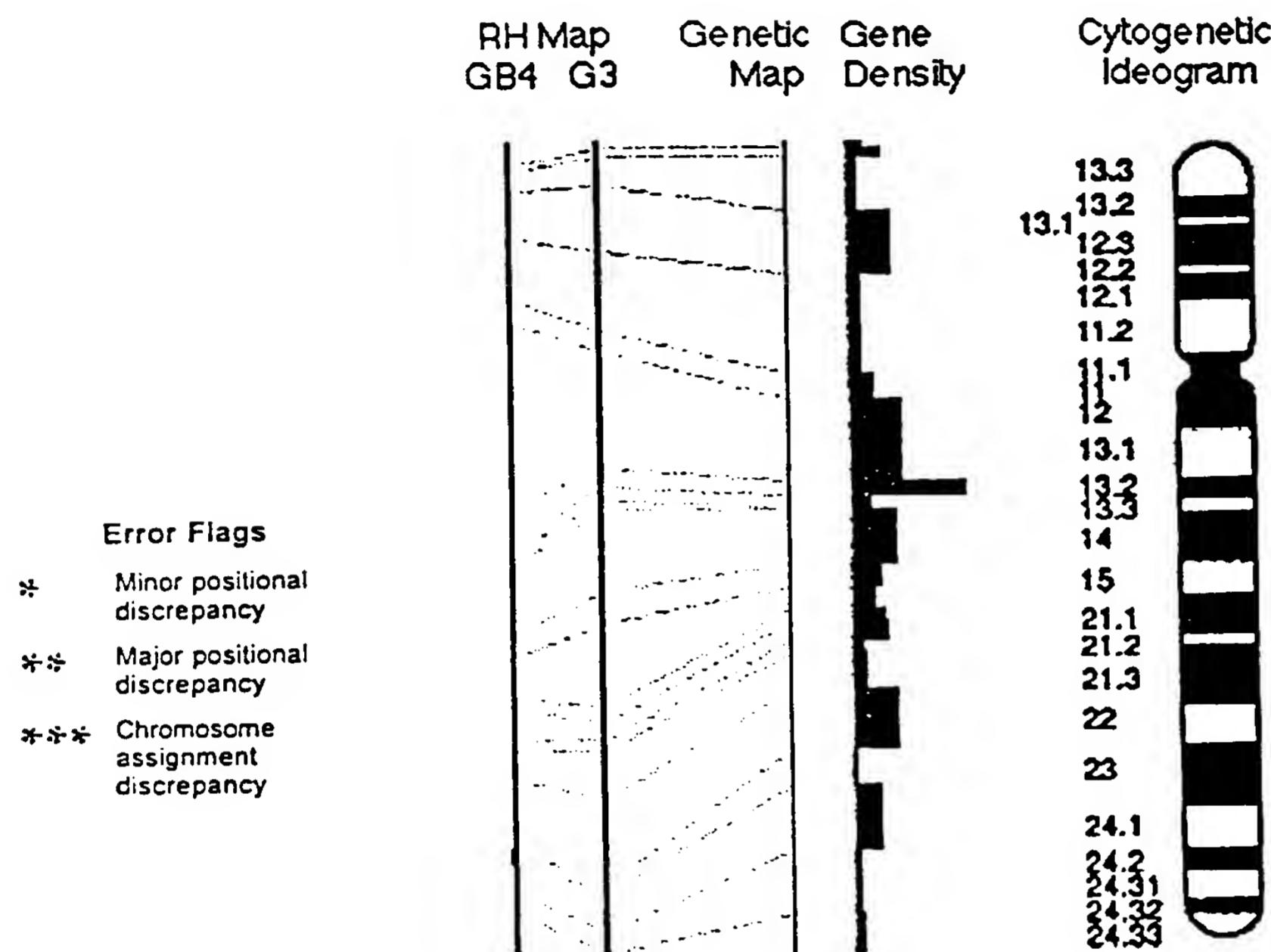


**FIG. 1D**

High Specific IgE & Asthma



## Chromosome 12: D12S79-D12S366



### About This Interval

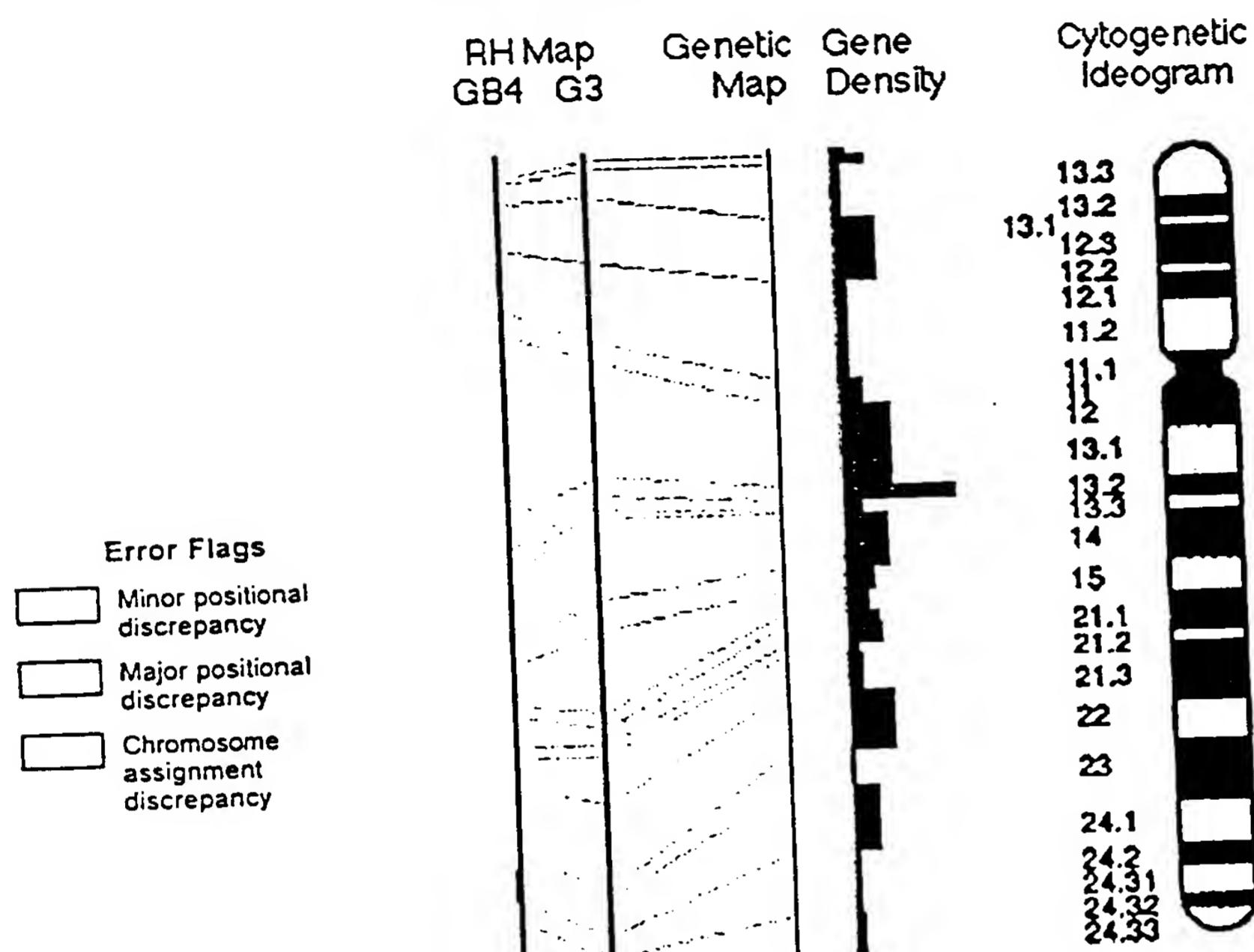
Top of interval: D12S79 (126.1 cM)  
Bottom of interval: D12S366 (133.8 cM)  
Genetic size of bin: 8 cM  
Physical size of bin: 9 cR3000

**FIG. 2 A**

 <b>126.1</b> <b>133.8</b>	<b>451.62 F</b> <b>454.24 P0.10</b> <b>455.39 P0.37</b> <b>455.39 P1.15</b> <b>455.70 P0.06</b> <b>455.81 P1.35</b> <b>455.86 P2.06</b> <b>456.02 P2.38</b> <b>456.34 P0.23</b> <b>456.34 P0.04 *</b> <b>456.86 P2.34</b> <b>456.86 P&gt;3.00</b> <b>456.86 "</b> <b>456.96 P1.66 *</b> <b>456.96 P0.04</b> <b>457.17 P1.31</b> <b>457.17 P0.13</b> <b>457.17 P0.30</b> <b>457.17 P0.38</b> <b>457.17 P0.31</b> <b>457.17 P0.18</b> <b>457.17 P1.35</b> <b>457.17 "</b> <b>457.27 P&gt;3.00 *</b> <b>457.27 P0.10 *</b> <b>457.48 P0.20</b> <b>460.94 P0.00 *</b> <b>460.94 F</b>	<b>AFM067yc5</b> <b>A009F32</b> <b>sts-N33343</b> <b>SGC38179</b> <b>stSG54526</b> <b>stSG1522</b> <b>sts-T56610</b> <b>sts-R33659</b> <b>sts-D29101</b> <b>SGC44506</b> <b>NIB1804</b> <b>stSG44263</b> <b>stSG62560</b> <b>sts-AA001615</b> <b>sts-T94297</b> <b>stSG54365</b> <b>WI-21497</b> <b>WI-20357</b> <b>SGC31491</b> <b>RK903_904</b> <b>sts-AA007571</b> <b>stSG46223</b> <b>stSG58387</b> <b>Cda1ce05</b> <b>sts-W79390</b> <b>sts-Z40829</b> <b>A005Q47</b> <b>AFM351tb9</b> <b>D12S366</b>	<b>D12S79</b> <b>KIAA0331</b> <b>ESTs</b> <b>ESTs</b> <b>ESTs</b> <b>ESTs</b> <b>Homo sapiens mRNA for KIAA0875 protein, p..</b> <b>EST</b> <b>EST</b> <b>ESTs</b> <b>ESTs, Weakly similar to calcium-binding pr..</b> <b>Homo sapiens clone 24852 mRNA sequence</b> <b>ESTs</b> <b>ESTs, Weakly similar to TBX2 gene [H.sapi..</b> <b>ESTs</b> <b>Homo sapiens mRNA for KIAA0875 protein, p..</b> <b>Homo sapiens mRNA for KIAA0875 protein, p..</b> <b>nitric oxide synthase 1 (neuronal)</b> <b>nitric oxide synthase 1 (neuronal)</b> <b>ESTs</b> <b>ESTs</b> <b>ESTs</b> <b>Homo sapiens clone 23714 mRNA sequence</b> <b>non-metastatic cells 2, protein (NM23B) exp..</b> <b>ESTs</b> <b>ESTs</b> <b>Microsatellite anchor marker AFM351tb9</b>
			↑ Next interval up
			↓ Next interval down

**FIG. 2 B**

## Chromosome 12: D12S366-D12S340



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

### About This Interval

Top of interval: D12S366 (133.8 cM)

Bottom of interval: D12S340 (147.5 cM)

Genetic size of bin: 14 cM

Physical size of bin: 21 cR3000

133.8	◆ 460.94 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9
	462.85 P1.00 *	stSG8109		ESTs
	462.85 "	sts-X75252	PBP	prostatic binding protein
	462.95 P1.04	sts-AA011374		Homo sapiens KIAA0431 mRNA, partial cds

FIG. 2 C

463.77 P0.19	WI-16745		Human clone 37, 5cM region surrounding hep...
◆ 463.77 P0.20	SGC33949	KIAA0262	KIAA0262 gene product
463.98 P0.02	A008B04		ESTs
463.98 "	stSG50309		ESTs
463.98 "	stSG49970		Homo sapiens mRNA for KIAA0875 protein, p..
463.98 P0.04	stSG27318		Human clone 23932 mRNA sequence
463.98 P0.08	R06295		EST
463.98 P1.33	sts-W56792		ESTs
464.08 P2.32	A007E48		ESTs
464.19 P1.28	A009U43		ESTs
464.29 P1.33	stSG3138		Homo sapiens mRNA for KIAA0949 protein, p..
464.39 P1.09	sts-F21636		Human DNA sequence from BAC 15E1 on chrom..
464.39 P1.13	stSG15685	KIAA0262	KIAA0262 gene product
464.39 "	RP_P0_1	RPLP0	Ribosomal protein large, P0
464.39 P1.09	stSG29626		ESTs
464.39 P1.14	stSG31407		Human DNA sequence from BAC 15E1 on chrom..
464.39 "	A001T32	PXN	paxillin
464.39 "	A001W18		H.sapiens mRNA for AMP-activated protein ..
464.39 "	WIAF-40		Human mRNA for KIAA0219 gene, partial cds
464.39 "	sts-T95105		ESTs
464.39 "	Cda0id01		ESTs
464.39 P1.13	stSG31431		ESTs, Moderately similar to (defline not a..
◆ 464.39 " *	WI-13177		Homo sapiens clone 23714 mRNA sequence
464.39 "	IB1092		Homo sapiens clone 23714 mRNA sequence
464.39 "	T79466		ESTs
464.39 P1.18	stSG48379		ESTs
464.45 P1.05	KIAA0219		Human mRNA for KIAA0219 gene, partial cds
464.45 "	stSG40392		ESTs
464.45 "	stSG31586		H.sapiens mRNA for AMP-activated protein ..
◆ 464.49 P0.21	A006F12	KIAA0152	KIAA0152 gene product
464.49 P0.25	sts-AA002185	PXN	paxillin
464.49 P0.10	stSG48442		ESTs
464.49 "	sts-T16456		ESTs
464.49 "	stSG62260		ESTs

FIG. 2 D

	464.49 "	NIB1331		ESTs
	464.49 "	WI-15518		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49 "	WIAF-1058		ESTs, Moderately similar to unknown [H.sap..
	464.49 "	SGC34758		ESTs
	464.49 "	WI-19738		Homo sapiens mRNA for KIAA0787 protein, p..
	464.49 "	IB383		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49 "	SGC32343		ESTs
	464.79 P0.96	SGC33521		ESTs
	464.79 P0.96 *	X58965	NME2	non-metastatic cells 2, protein (NM23B) exp..
	465.20 P0.20	sts-H10302		ESTs
◆	465.38 P0.85	A007E11	KIAA0262	KIAA0262 gene product
	465.41 P0.81	A007I44	RPLP0	ribosomal protein, large, P0
	465.41 "	stSG22726.		EST
	465.41 "	WI-17776		ESTs
	465.41 "	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41 "	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41 P0.77	stSG4775	SFRS9	splicing factor, arginine/serine-rich 9
	465.41 "	A002J47		ESTs, Weakly similar to heat shock protein..
	465.41 P0.80	stSG46660		EST
	465.51 P0.75	stSG41086	PXN	paxillin
	465.51 P0.83	stSG52121		ESTs
	465.91 P0.01	WI-16071		ESTs
	465.91 P0.00	WI-13962		H.sapiens mRNA for AMP-activated protein ..
	466.62 P0.00	sts-AA011220	SFRS9	splicing factor, arginine/serine-rich 9
	466.71 P0.00	stSG4712		ESTs, Weakly similar to homology with o251..
	466.91 P0.01	WI-15135		Homo sapiens mRNA for KIAA0787 protein, p..
	466.91 P0.01	D12S2088	TCF1	transcription factor 1, hepatic; LF-B1, hep..
	467.01 P0.01	stSG52567		ESTs
135.1	467.11 F	AFM123xh2	D12S86	Microsatellite marker AFM123xh2
135.1	467.11 P0.01	AFM299zd5	D12S349	Microsatellite marker AFM299zd5
	467.11 P0.01	AFM123xh2		Unknown
137.5	◆ 467.21 P0.02	AFM220zf4	D12S321	Microsatellite marker AFM220zf4
	467.21 P0.02	sts-W73277	SFRS9	splicing factor, arginine/serine-rich 9
	467.21 P0.02	stSG8721		EST

FIG. 2 E

467.21 "	stSG44224		ESTs
467.21 "	stSG49978		H.sapiens mRNA for AMP-activated protein ..
◆ 467.21 "	stSG31862		Homo sapiens HSPC004 mRNA, complete cds
467.21 "	stSG47820		ESTs
467.21 "	Bdac4h06	KIAA0262	KIAA0262 gene product
467.21 "	stSG15021		ESTs
467.21 "	A002B13	SFRS9	splicing factor, arginine/serine-rich 9
◆ 467.21 "	HS0549	KIAA0262	KIAA0262 gene product
467.21 P0.03	SGC35167		EST
467.21 P0.03	WI-19637		H.sapiens mRNA for AMP-activated protein ..
467.21 P0.02	WIAF-607		Unknown
467.31 P0.02	WI-16997	RPLP0	ribosomal protein, large, P0
468.93 P0.85	SGC31344		EST
469.13 P0.90	A007C39	ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 ..
469.13 P0.14	stSG35104		ESTs
469.13 "	A006Q41		Unknown
469.23 P0.18	sts-Y07684	P2RX4	purinergic receptor P2X, ligand-gated ion c..
469.33 P0.93	stSG8506		ESTs, Moderately similar to unknown [H.sap..]
469.33 "	R01708		EST
469.33 "	stSG54819	HCALB_BR	calbrain
469.33 "	A001Z45		ESTs, Highly similar to (defline not avail..)
469.33 "	stSG35318		ESTs, Weakly similar to fos39554 1 [H.sapi..]
469.33 "	stSG63173		EST
469.33 "	stSG31374	OASL	2'-5'oligoadenylate synthetase-like
469.42 P1.01	WI-16068		EST
469.44 P0.23	stSG1961		Homo sapiens mRNA for KIAA0787 protein, p..
469.44 "	stSG62627		EST
469.44 "	stSG36007		Homo sapiens full length insert cDNA clone..
469.44 "	stSG39281	P2RX7	purinergic receptor P2X, ligand-gated ion c..
469.44 "	stSG2554		Homo sapiens mRNA for KIAA0787 protein, p..
469.44 "	stSG62591		ESTs
◆ 469.54 P1.03	A006N38	KIAA0152	KIAA0152 gene product
469.62 P1.03	sts-N34573		ESTs
469.62 P1.03	sts-N58045		ESTs

FIG. 2 F

469.62 P1.04	WI-13224		EST
469.83 P1.12	SGC34424		ESTs
469.93 P1.14	stSG3875	PSMD9	proteasome (prosome, macropain) 26S subunit..
470.14 P1.17	stSG52516		ESTs, Weakly similar to (defline not avail..
470.24 P1.32	D0S1735E		ESTs
470.24 P1.12	WI-6178		ESTs
470.32 P1.25	sts-U29895		Unknown
470.32 P1.24	WI-19611	PSMD9	proteasome (prosome, macropain) 26S subunit..
470.43 P1.29	stSG52094		ESTs
470.63 P1.38	A004O17		ESTs
◆ 470.77 P1.32	** SGC33451		ESTs, Weakly similar to rhoHP1 [H.sapiens..
◆ 470.84 P1.35	** sts-X64838	RSN	restin (Reed-Steinberg cell-expressed inter..
470.84 P1.52	WI-13062		Homo sapiens mRNA, expressed in fibroblast..
471.27 P1.60	sts-R99269		EST
471.37 P1.70	stSG1991		ESTs
471.37 "	stSG15859		Homo sapiens full length insert cDNA YQ02..
471.58 P1.78	stSG29729		ESTs, Weakly similar to (defline not avail..
471.58 P1.37	WI-16979		ESTs
471.65 P1.39	WI-17693		EST
471.80 P1.29	WI-22060		ESTs
471.90 P>3.00	stSG8210		ESTs, Moderately similar to neuronal threa..
471.90 "	WI-17956		EST
471.90 "	WI-20969		Homo sapiens mRNA for KIAA0867 protein, c..
471.90 "	stSG47029		ESTs
471.90 "	stSG47647		EST
471.90 "	sts-W45376		Homo sapiens mRNA for KIAA0867 protein, c..
◆ 471.90 "	** WI-6021	RSN	restin (Reed-Steinberg cell-expressed inter..
471.90 "	NIB962		ESTs
471.90 "	A009E34		ESTs, Moderately similar to neuronal threa..
471.90 "	sts-T17477		ESTs
472.08 P1.49	sts-X89984		H.sapiens mRNA for BCL7A protein
472.12 P>3.00	SGC34693		EST
472.12 P>3.00	A009O01		ESTs, Weakly similar to neuronal thread pr..
472.29 P>3.00	stSG47084		ESTs

FIG. 2 G

472.40 P>3.00	stSG58209	EEF1D	eukaryotic translation elongation factor 1 d..
472.40 P>3.00	AA213821	EEF1D	eukaryotic translation elongation factor 1 d..
472.61 P>3.00	A002R44		Unknown
472.61 P>3.00	SGC35850	EEF1D	eukaryotic translation elongation factor 1 d..
472.72 P0.01	sts-H98108		ESTs
472.97 P>3.00	WI-6239		ESTs
473.04 P>3.00	sts-H75490		ESTs
◆ 473.58 P>3.00 **	WI-14983	RSN	restin (Reed-Steinberg cell-expressed inter..
474.01 P>3.00	stSG8610		ESTs
474.01 P>3.00	stSG47080		ESTs
474.38 P2.18	stSG8686		ESTs, Weakly similar to similar to pre-mRN..
474.38 P2.25	stSG26358		ESTs, Weakly similar to similar to pre-mRN..
474.38 "	stSG29931		ESTs
474.38 "	WI-17926		ESTs
474.38 "	WI-12790		ESTs, Weakly similar to MULTIDRUG RESI..
474.38 "	1834		EST
474.38 P2.26	sts-X98258	MPP-9	M phase phosphoprotein 9
474.38 P2.39	stSG40753		ESTs
474.64 P>3.00	A004D47		ESTs, Highly similar to There are three pu..
474.64 P>3.00	sts-N23129	MPP-9	M phase phosphoprotein 9
474.75 P2.41	sts-AA040696		ESTs
474.81 P2.37	sts-AA022496		ESTs
474.81 P2.28	stSG46930	MPP-9	M phase phosphoprotein 9
474.97 P>3.00	WI-20552	DRP	density-regulated protein
475.02 P>3.00	SGC30324		ESTs
475.07 P>3.00	D10923	HM74	putative chemokine receptor, GTP-binding pr..
475.07 P>3.00	stSG2418	DOC1	Deleted in oral cancer-1
475.07 "	stSG21321		ESTs
475.07 "	stSG53515	MPP-9	M phase phosphoprotein 9
475.07 P>3.00	SGC31687	DOC1	Deleted in oral cancer-1
475.07 P>3.00	WIAF-214	HM74	putative chemokine receptor, GTP-binding pr..
475.13 P0.79	sts-W93806		ESTs
475.13 P2.13	stSG48145		ESTs
475.18 P2.34	A003B12		Homo sapiens full length insert cDNA clone..

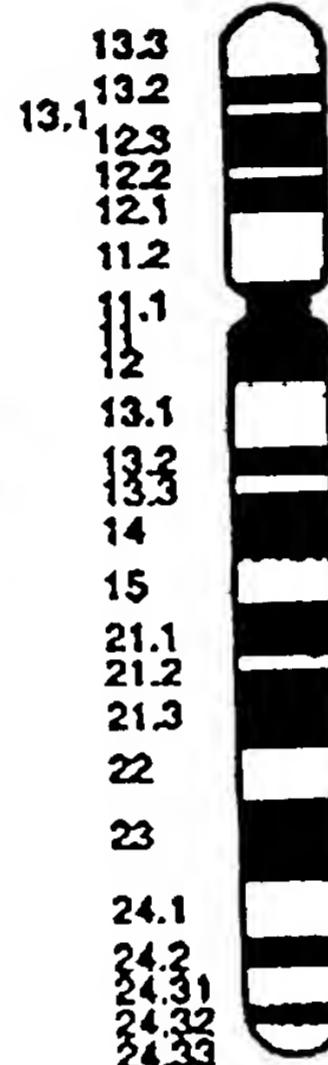
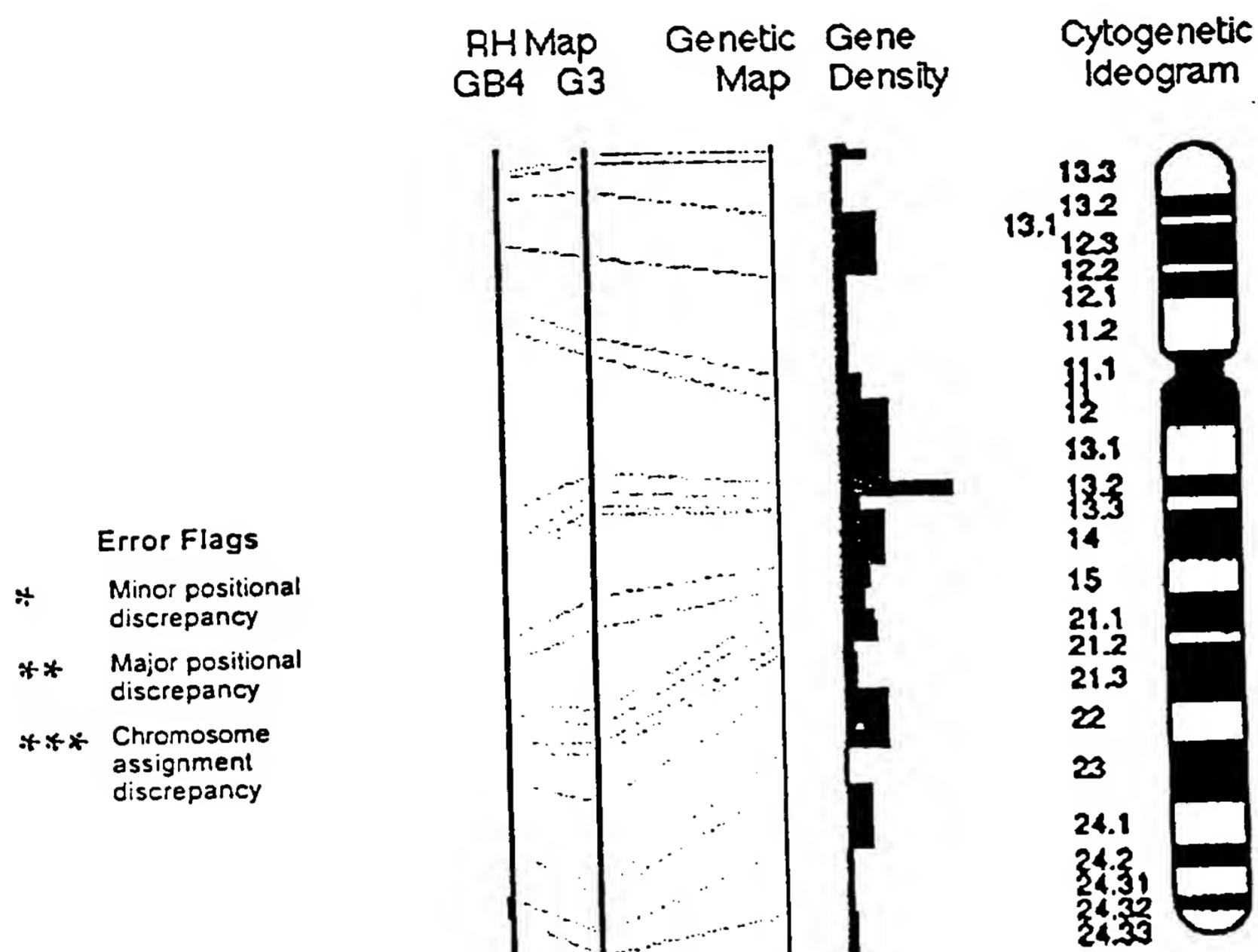
FIG. 2 H

475.18 P>3.00	WI-22211		Homo sapiens full length insert cDNA clone..	
475.18 P2.08	stSG48093		ESTs	
475.18 "	A004P27		ESTs, Weakly similar to MULTIDRUG RESI..	
475.35 P2.10	stSG9904		ESTs	
475.40 P0.45	sts-AA024696		ESTs	
475.51 P>3.00	stSG53793		ESTs	
476.10 P>3.00	Bda98d05		Homo sapiens full length insert cDNA clone..	
476.21 P>3.00	sts-H24468		ESTs	
476.21 P>3.00	sts-N94741		ESTs	
476.64 P0.28	stSG22488		ESTs	
476.85 P0.36	stSG44909		ESTs	
477.06 P0.10	stSG54797		ESTs	
477.27 P1.33	stSG48099		ESTs	
477.37 P0.09 *	sts-AA028894		Homo sapiens silencing mediator of retinoic..	
477.80 P1.44	stSG52727		EST	
477.80 "	U44799		Human U1-snRNP binding protein homolog mR..	
477.80 "	WI-15963		ESTs	
477.80 "	stSG53886		ESTs, Weakly similar to neuronal thread pr..	
478.74 P0.01	WIAF-364		ESTs	
479.01 P0.21	WI-21080		ESTs	
479.13 P0.19	A009B29		ESTs	
479.33 P0.22	A006F32	EIF2B1	eukaryotic translation initiation factor 2B..	
479.33 P0.19	WIAF-449	EIF2B1	eukaryotic translation initiation factor 2B..	
479.33 P0.19 *	WI-15890		H.sapiens mRNA for transmembrane protein r..	
479.55 P0.20 *	stSG349		H.sapiens mRNA for transmembrane protein r..	
479.55 "	*	A004O46	BDKRB2	bradykinin receptor B2
479.55 "	stSG42540		ESTs	
479.55 "	sts-N26791		ESTs	
479.55 "	stSG53943		ESTs	
479.55 "	stSG49468		EST	
145.7	479.74 P0.16	AFM294ze9	D12S342	Microsatellite marker AFM294ze9
	481.46 P0.00	sts-AA007694		EST
147.5	= ♀ 481.56 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1

Next interval down

FIG. 2 I

## Chromosome 12: D12S340-D12S97



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

### About This Interval

Top of interval: D12S340 (147.5 cM)

Bottom of interval: D12S97 (160.9 cM)

Genetic size of bin: 13 cM

Physical size of bin: 13 cR3000

147.5	Next interval up	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1
481.56 F		SGC31838		ESTs
481.66 P0.00		stSG48255		ESTs
483.18 P0.70		stSG47315		ESTs
483.58 P0.69				

FIG. 2 J

483.87 P0.83	stSG47707		ESTs
484.70 P0.93	stSG4060		ESTs
484.70 "	stSG62390	GTF2H3	general transcription factor IIH, polypepti..
484.70 "	stSG42994		ESTs
484.73 P0.74	stSG46906		ESTs
484.80 P0.91	A004X33		ESTs
484.91 P1.11	stSG3211		ESTs, Weakly similar to B-cell growth fact.
484.91 " *	sts-Z41302	BDKRB2	bradykinin receptor B2
484.91 " *	sts-Z41302	BDKRB2	bradykinin receptor B2
484.91 "	sts-T58259		ESTs, Weakly similar to B-cell growth fact..
484.91 "	stSG52737		ESTs
484.91 "	Bda03b10	UBC	ubiquitin C
484.91 "	stSG1936	CD36L1	CD36 antigen (collagen type I receptor, thr..
484.91 "	sts-AA017225		ESTs
484.91 P1.15	WI-12212		ESTs
485.12 P1.18	A004F14		ESTs
485.12 P1.18	SGC31333		ESTs
485.23 P1.21 *	WI-12482	BDKRB2	bradykinin receptor B2
485.23 P1.07	sts-AA017698		ESTs
485.33 P1.22	WI-12422		ESTs
485.51 P1.18	stSG42398		EST
485.64 P1.04	sts-AA009669		ESTs
486.07 P2.50	stSG21539		EST
486.13 P1.44	WI-12439		EST
486.34 P1.26	sts-W31616	UBC	ubiquitin C
486.38 P>3.00	stSG54715		ESTs
486.76 P1.64 *	WI-6921		H.sapiens mRNA for transmembrane protein r..
487.08 P>3.00	WI-13120		Human mRNA for KIAA0318 gene, partial cds
487.23 P>3.00	stSG54353		ESTs
487.23 P>3.00	stSG22703		EST
487.28 P>3.00	stSG62698		ESTs
487.28 P>3.00 *	sts-D60472		Homo sapiens silencing mediator of retinoic..
487.28 P>3.00	stSG36097		ESTs
487.33 P1.36	sts-U37146		Homo sapiens silencing mediator of retinoic..

FIG. 2 K

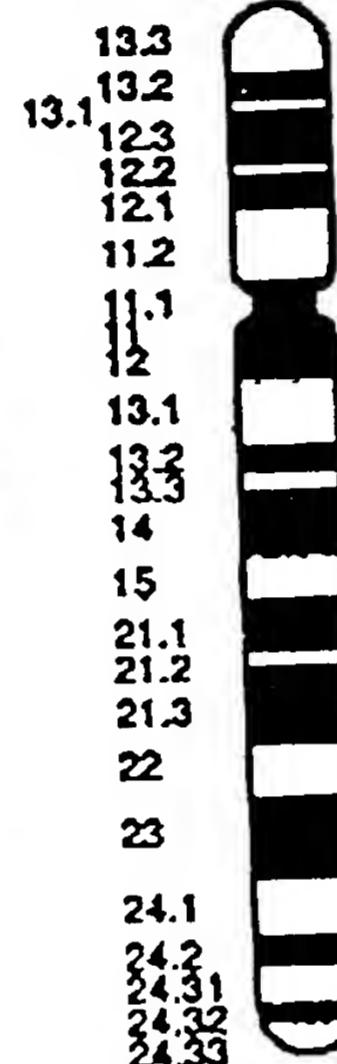
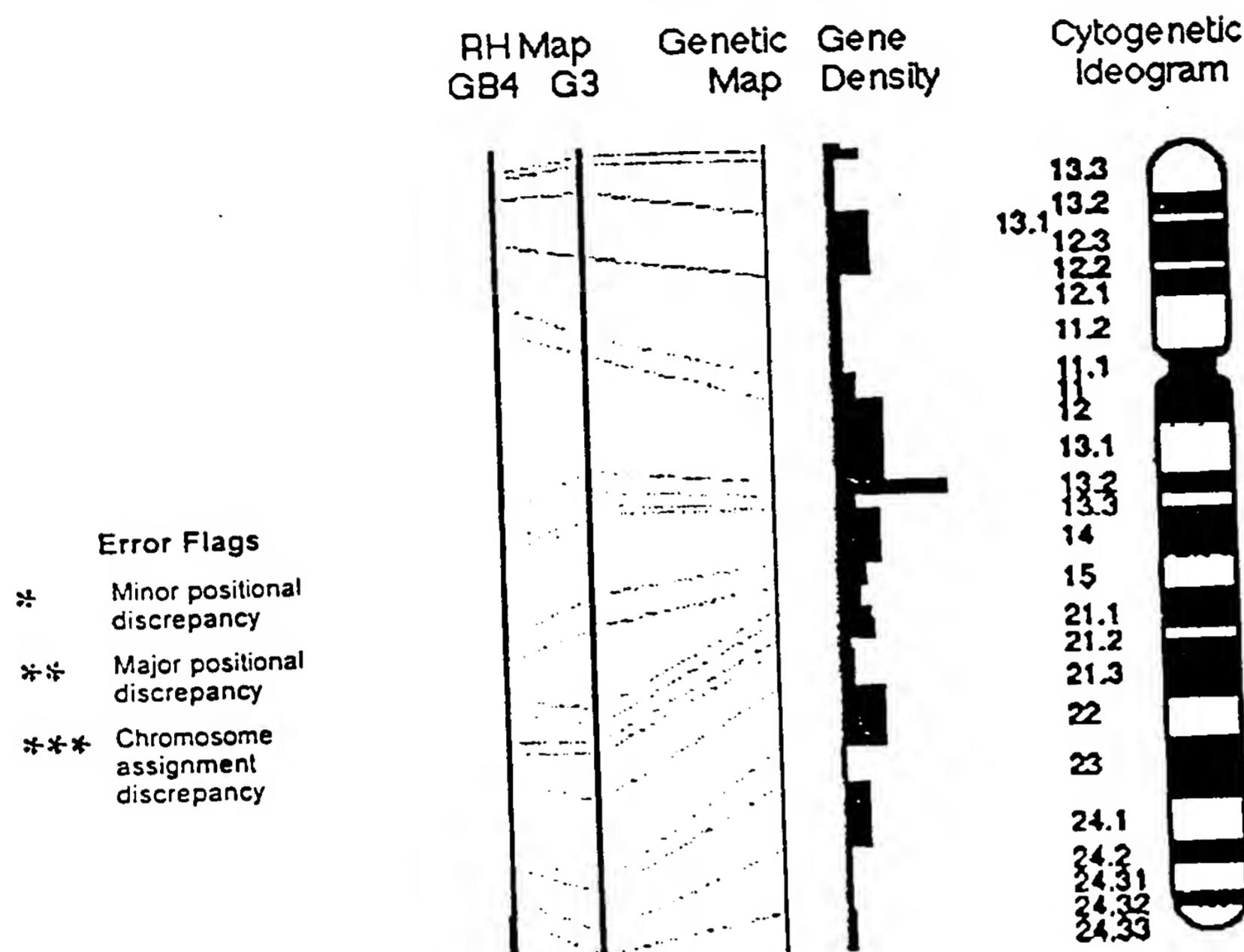
	487.50 P>3.00	stSG9807	ESTs
	487.50 P>3.00	stSG15434	ESTs
	487.60 P>3.00	stSG53251	ESTs
	487.60 P>3.00	stSG30525	SRRP129 SC35-interacting protein 1
	487.60 P>3.00	stSG46424	ESTs
	487.70 P>3.00	A007A34	ESTs
154.4	487.75 P2.00	AFMa197zd9	D12S1609 Microsatellite marker AFMa197zd9
	487.75 P2.02	A006D44	ESTs
	487.80 P>3.00	SGC30248	ESTs, Weakly similar to peptide/histidine ..
	488.07 P1.68	stSG6320	Homo sapiens clone 24617 mRNA sequence
	488.07 P1.66	stSG6305	Homo sapiens clone 24790 mRNA sequence
	488.07 P0.02	sts-N20163	Homo sapiens full length insert cDNA clone..
	488.12 P>3.00	stSG60065	ESTs
	488.12 P>3.00	stSG47723	ESTs
	488.44 P1.59	stSG3292	Homo sapiens clone 24790 mRNA sequence
	488.44 P0.03	WIAF-856	EST, Weakly similar to reverse transcripta..
	488.65 P1.54	WI-12272	Homo sapiens clone 24790 mRNA sequence
	488.65 P1.82	stSG52343	ESTs
	488.82 P1.80	stSG16387	CPN2 carboxypeptidase N, polypeptide 2, 83kD
	488.97 P1.80	SGC31722	ESTs
	489.07 P0.06	stSG54325	ESTs
	489.07 P>3.00	stSG63473	ESTs
160.9	♦ 489.07 P>3.00	AFMa123xel	D12S367 Microsatellite marker AFMa123xel
	489.14 P0.17	sts-T81113	ESTs
	489.29 P0.05	sts-AA025438	EST
	489.50 P1.37	***	Cdalad08 ESTs
	489.50 P0.05	WI-15018	ESTs
	489.50 P1.50	WI-18492	ESTs
	489.57 P1.48	WI-16177	Homo sapiens androgen receptor associated p..
	489.67 P1.44	stSG53307	ESTs
	489.71 P1.43	stSG53541	Homo sapiens hiwi mRNA, partial cds
	489.71 P1.43	stSG9546	Homo sapiens clone 24617 mRNA sequence
	489.89 P1.56	A006O16	ESTs
	490.10 P1.42	H64839	EST

FIG. 2 L

160.9 | 490.20 P0.05      stSG43910      SFRS8      splicing factor, arginine/serine-rich 8 (sup..  
       ♦ 494.19 F      AFM210zd6      D12S97      Microsatellite anchor marker AFM210zd6  
       Next interval down

FIG. 2 M

## Chromosome 12: D12S97-qTEL



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

### About This Interval

Top of interval: D12S97 (160.9 cM)

Bottom of interval: chr12\_qTEL (169.1 cM)

Genetic size of bin: 8 cM

Physical size of bin: 172 cR3000

160.9	◆ 494.19 F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6
	498.06 P0.02	stSG53600		ESTs, Weakly similar to peptide/histidine ..
	499.71 P1.73	stSG3357		ESTs
165.7	499.71 "	AFM295ye9	D12S343	Microsatellite marker AFM295ye9

FIG. 2 N

499.71 P1.72	stSG30906		ESTs
499.71 "	stSG43796	MMP17	matrix metalloproteinase 17 (membrane-insert..
499.71 P1.71	sts-X89576	MMP17	matrix metalloproteinase 17 (membrane-insert..
499.92 P>3.00	stSG43769		ESTs
500.50 P1.88	stSG26056		ESTs
500.50 P2.33	SGC30786	KIAA0331	KIAA0331 gene product
500.61 P>3.00	stSG1702		Homo sapiens CAGH32 mRNA, partial cds
500.61 "	sts-N59820		ESTs
500.61 "	stSG42115	KIAA0331	KIAA0331 gene product
500.61 "	IB2452	ULK1	unc-51 (C. elegans)-like kinase 1
500.61 "	stSG52521		ESTs
500.61 "	FB9F8		ESTs, Weakly similar to PUTATIVE ATP-D..
500.61 "	AA252357		ESTs
500.61 "	stSG4720		Homo sapiens pseudouridine synthase 1 (PUS..
500.61 "	sts-AA001424	KIAA0331	KIAA0331 gene product
500.61 P>3.00	stSG31443		ESTs
500.61 P>3.00	stSG49622	ULK1	unc-51 (C. elegans)-like kinase 1
500.61 P2.49	stSG50559		ESTs
501.04 P1.10	stSG54842		ESTs
501.04 P2.03	A008Y05		Unknown
501.89 P2.18	stSG39493		Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	A002A44		Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	sts-H94865		EST
501.99 P>3.00	R50113		ESTs
502.10 P1.75	stSG48386		ESTs
502.10 "	stSG50504		ESTs
502.63 P0.06	A006R19		ESTs
502.63 P1.06	WIAF-864		ESTs
502.94 P1.51	stSG54813		ESTs, Weakly similar to peroxisome membran..
503.04 P1.42	A004B47		ESTs, Highly similar to DNA polymerase ep..
503.25 P0.28	stSG27206		ESTs
503.25 "	stSG40199		Homo sapiens mRNA for KIAA0692 protein, p..
503.46 P0.23	stSG8935		ESTs
504.68 P0.69	stSG4731		Homo sapiens mRNA for KIAA0692 protein, p..

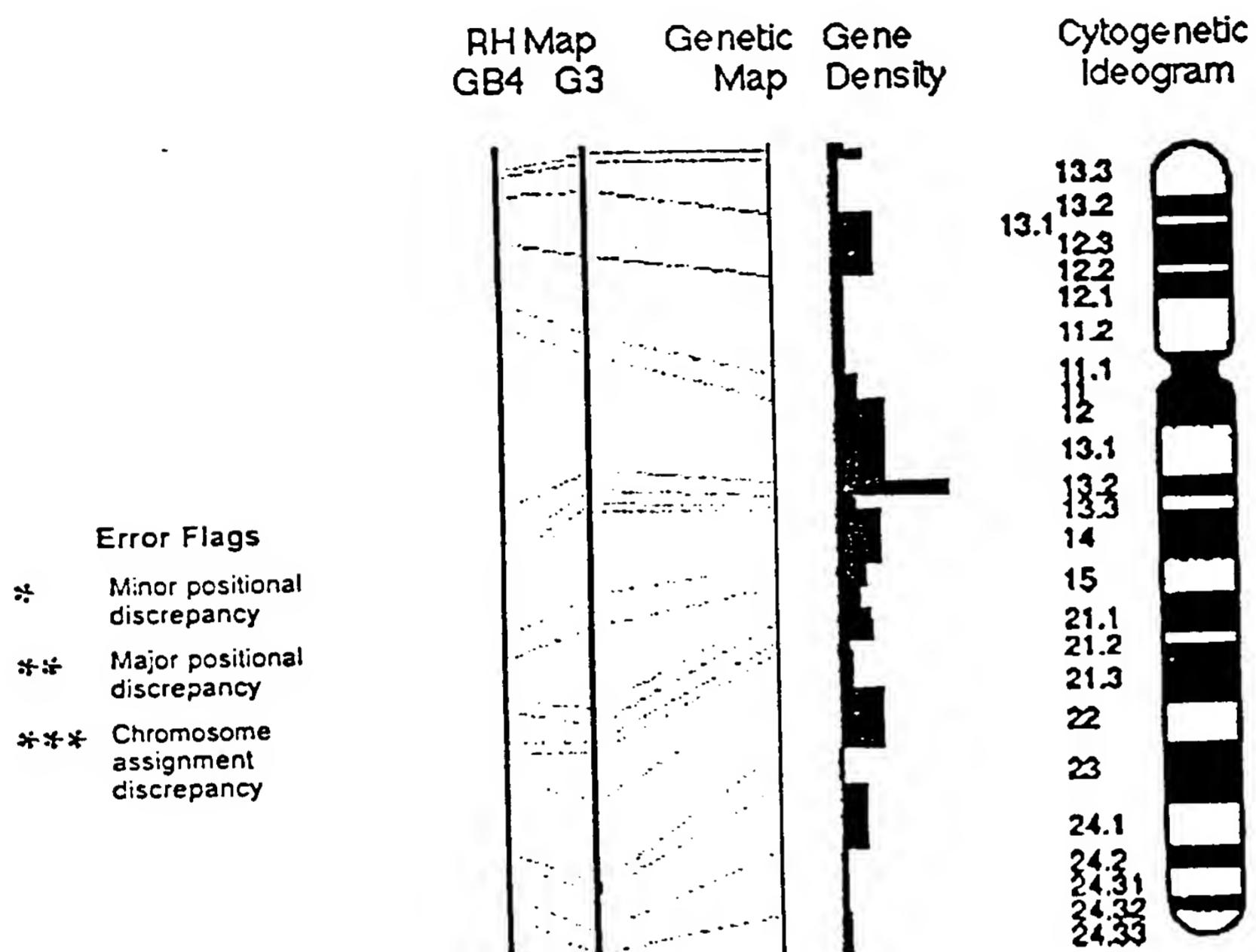
FIG. 2 O

	504.68 "	A005Q05	ESTs
	504.68 "	stSG8142	ESTs, Highly similar to DNA polymerase ep..
169.1	506.39 F	AFM310vd5	D12S357 Microsatellite marker AFM310vd5
	506.39 P0.02	A005X42	Homo sapiens mRNA for KIAA0692 protein, p..
	508.59 P0.78	Cda18g06	ESTs
◆	508.59 P0.78 **	Cda1jf08	Homo sapiens mRNA for GCP170, complete cd..
	508.59 P0.54	R39599	ESTs
	509.98 P0.10	stSG31494	ZNF140 zinc finger protein 140 (clone pHZ-39)
	509.98 P0.16	stSG40222	ESTs
	509.98 "	sts-R55615	ESTs, Weakly similar to zinc finger protei..
	509.98 "	sts-R02295	ESTs
	509.98 "	sts-R81342	ESTs
	511.20 F	TEL-12q82	Marker TEL-12q82
	512.81 P0.20	sts-H65839	ESTs, Weakly similar to transformation-rel..
	514.97 P0.36	stSG46141	ESTs, Weakly similar to zinc finger protei..
	514.97 P0.90	stSG52998	ESTs
	519.10 P1.77	A008W21	CYP51 cytochrome P450, 51 (lanosterol 14-alpha-de..
	519.54 P0.81	stSG52716	ESTs

TELOMERE

FIG. 2 P

## Chromosome 12: D12S79-D12S366



### About This Interval

Top of interval: D12S79 (126.1 cM)

Bottom of interval: D12S366 (133.8 cM)

Genetic size of bin: 8 cM

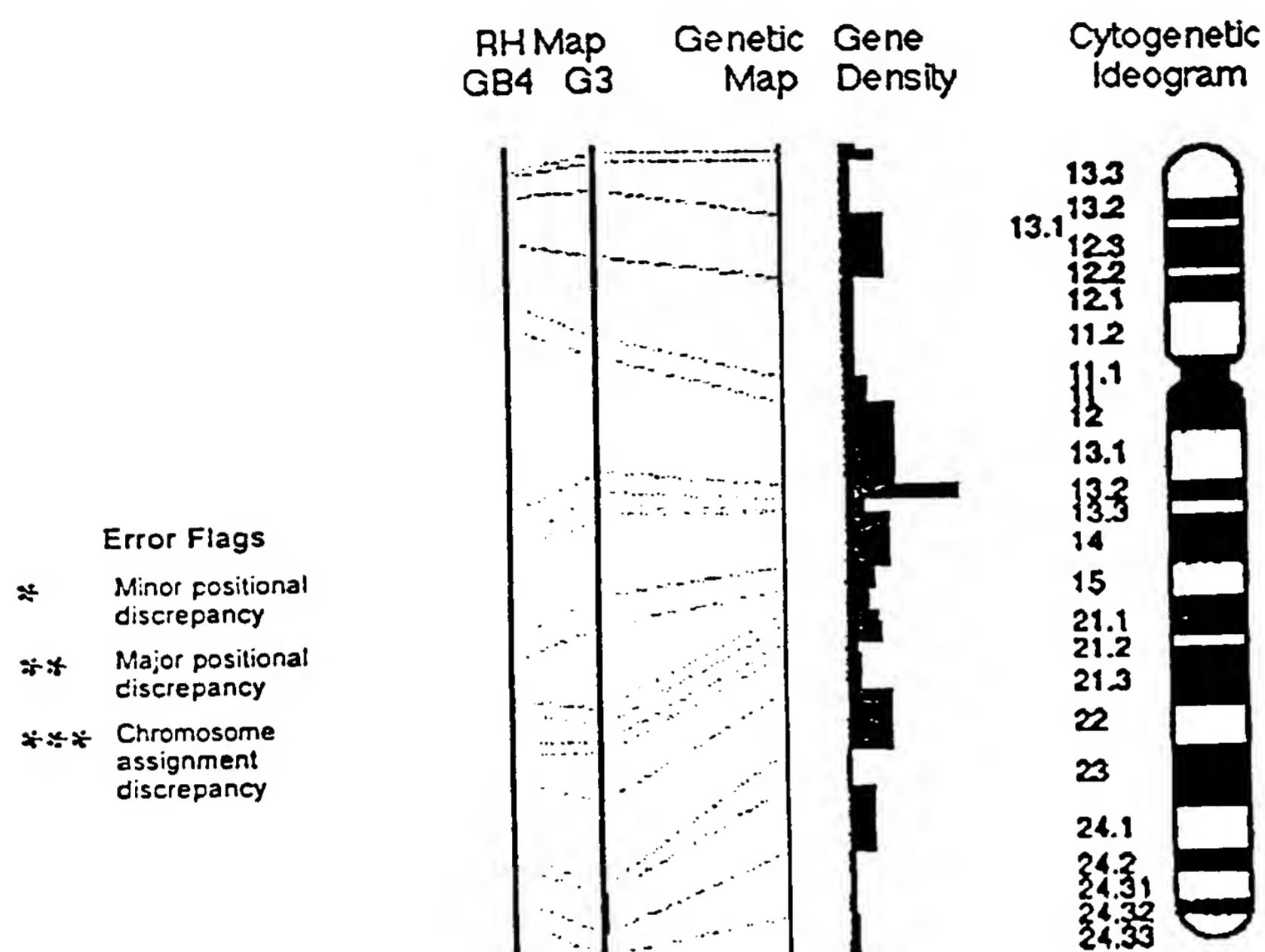
Physical size of bin: 63 cR<sub>10000</sub>

FIG. 3 A

		▲ Next interval up
126.1	◆ 4955 F	AFM067yc5 D12S79 Microsatellite anchor marker AFM067yc5 (SHGC-692)
129.2	4988 F	AFMa067wel D12S1718 Microsatellite marker AFMa067wel (SHGC-20..)
	◆ 5007 F *	SHGC-2657 Homo sapiens clone 23714 mRNA sequence
	◆ 5014 F *	SHGC-2653 Homo sapiens clone 23714 mRNA sequence
133.8	◆ 5018 F	AFM351tb9 D12S366 Microsatellite anchor marker AFM351tb9 (SHGC-2155)
		▼ Next interval down

FIG. 3 B

## Chromosome 12: D12S366-D12S340



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

### About This Interval

Top of interval: D12S366 (133.8 cM)

Bottom of interval: D12S340 (147.5 cM)

Genetic size of bin: 14 cM

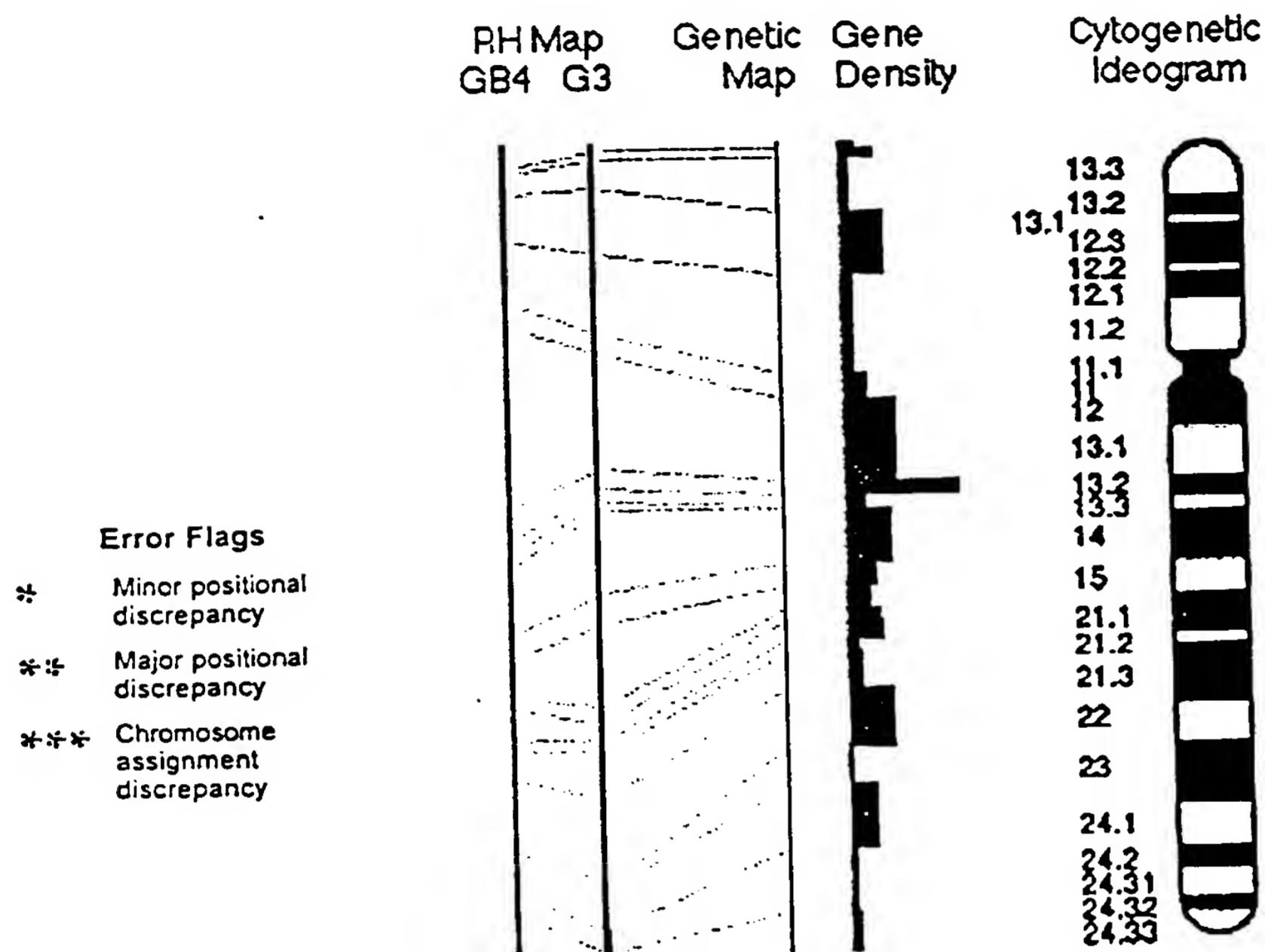
Physical size of bin: 261 cR<sub>10000</sub>

FIG. 3 C

			↑ Next interval up
133.8	◆ 5018 F	AFM351tb9	D12S366 Microsatellite anchor marker AFM351tb9 (SHGC-2155)
135.1	5047 F	AFMa225xe5	D12S1619 Microsatellite marker AFMa225xe5 (SHGC-20..)
	◆ 5085 F	SHGC-33949	KIAA0262 KIAA0262 gene product
	◆ 5089 F	SHGC-10488	KIAA0152 KIAA0152 gene product
	◆ 5093 F	SHGC-10346	Homo sapiens HSPC004 mRNA, complete cds
	◆ 5098 F	SHGC-13898	Homo sapiens HSPC004 mRNA, complete cds
137.5	◆ 5163 F	AFM220zf4	D12S321 Microsatellite marker AFM220zf4 (SHGC-212..)
	5199 F	SHGC-11702	ESTs
147.5	◆ 5279 F	AFM294xg1	D12S340 Microsatellite anchor marker AFM294xg1 (SHGC-2134)
		↓ Next interval down	

FIG. 3 D

## Chromosome 12: D12S340-D12S97



### Error Flags

- \* Minor positional discrepancy
- \*\* Major positional discrepancy
- \*\*\* Chromosome assignment discrepancy

The interval shown is on the G3 map

See also: equivalent interval on GB4 map

### About This Interval

Top of interval: D12S340 (147.5 cM)

Bottom of interval: D12S97 (160.9 cM)

Genetic size of bin: 13 cM

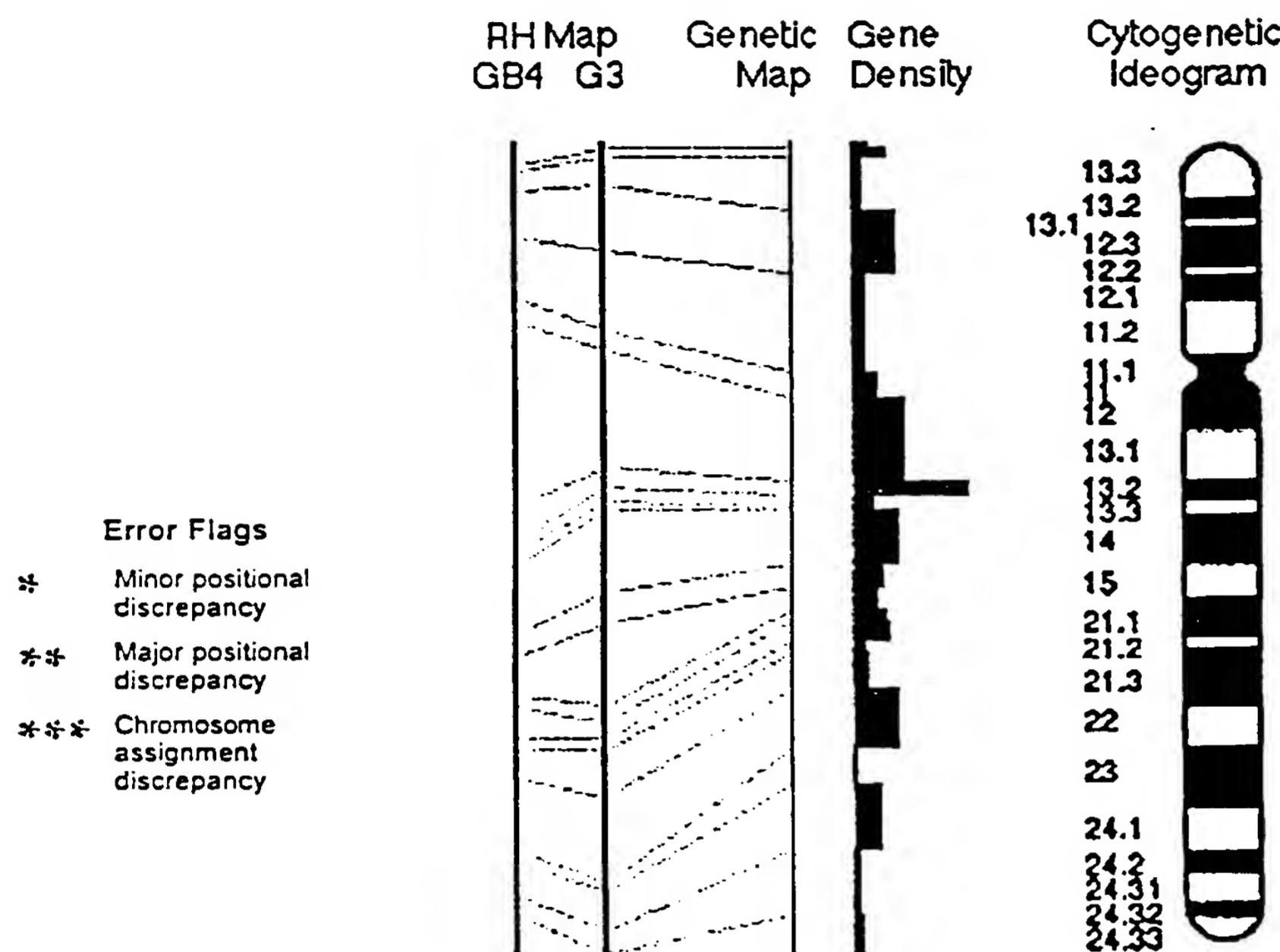
Physical size of bin: 151 cR<sub>10000</sub>

FIG. 3 E

Next interval up					
147.5	◆ 5279 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1 (SHGC-2134)	
148.3	5288 F	AFM234tb10	D12S324	Microsatellite marker AFM234tb10 (SHGC-21..)	
154.4	5316 F	AFMb350zb5	D12S1679	Microsatellite marker AFMb350zb5 (SHGC-20..)	
149.5	5358 F	AFM198wh2	D12S307	Microsatellite marker AFM198wh2 (SHGC-211..)	
157.2	5393 F	AFMb301we5	D12S1659	Microsatellite marker AFMb301we5 (SHGC-20..)	
160.9	◆ 5415 F	AFMa123xe1	D12S367	Microsatellite marker AFMa123xe1 (SHGC-21..)	
160.9	◆ 5430 F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6 (SHGC-372)	

FIG. 3 F

## Chromosome 12: D12S97-qTEL



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

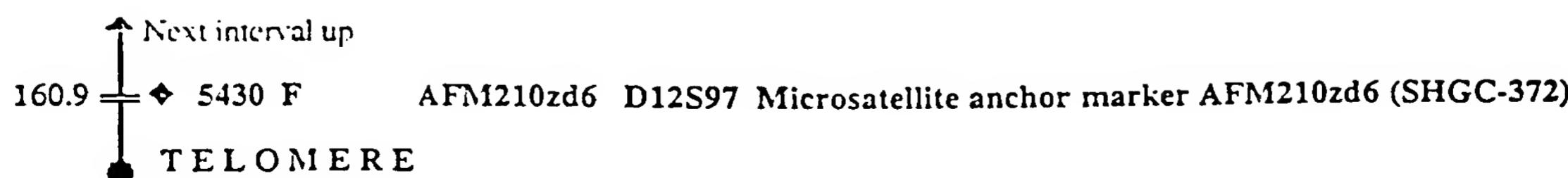
### About This Interval

Top of interval: D12S97 (160.9 cM)

Bottom of interval: chr12\_qTEL (169.1 cM)

Genetic size of bin: 8 cM

Physical size of bin: -4429 cR<sub>10000</sub>



**FIG. 3 G**

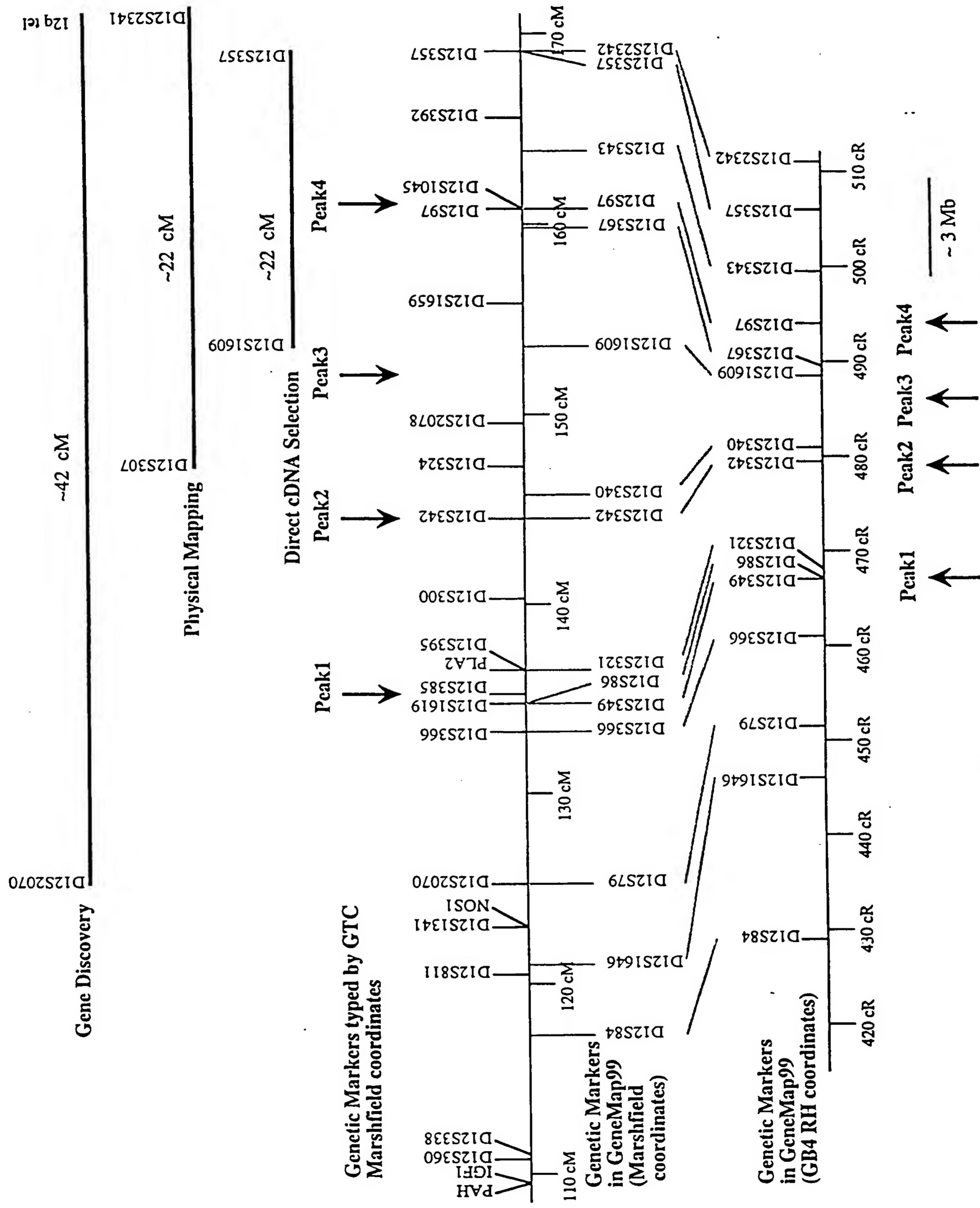
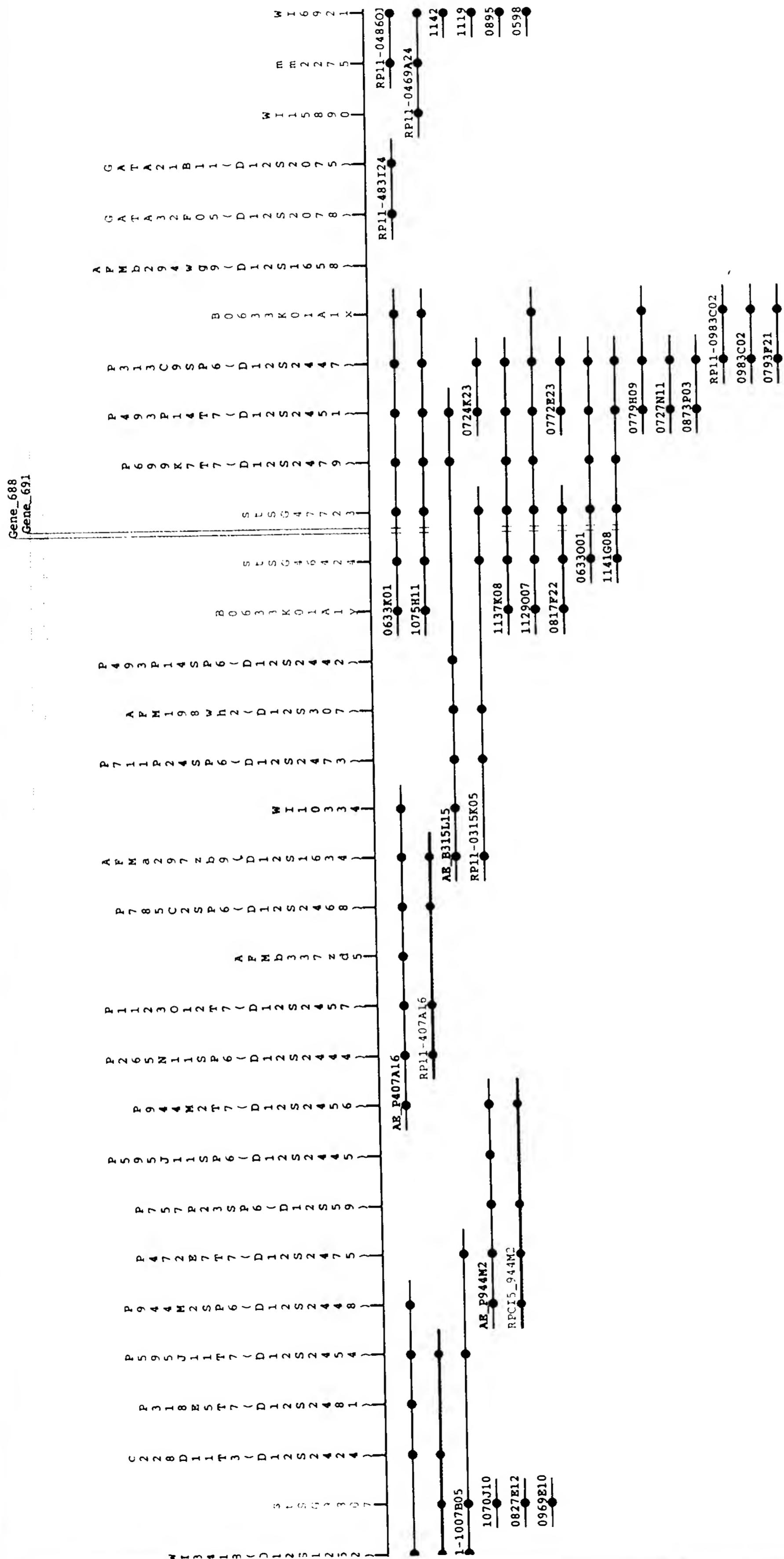
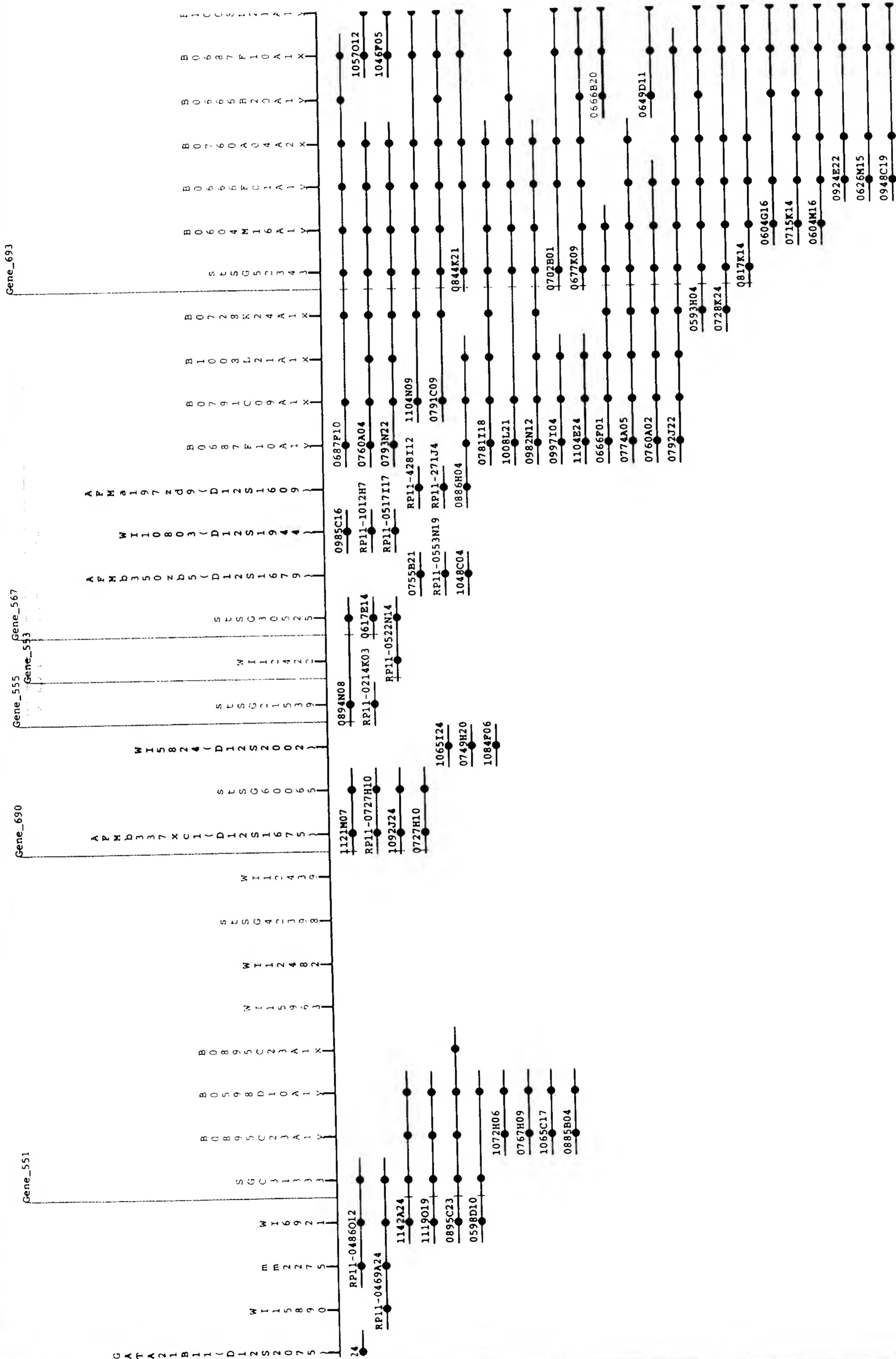


FIG. 4



**FIG. 5A**

**FIG. 5B**



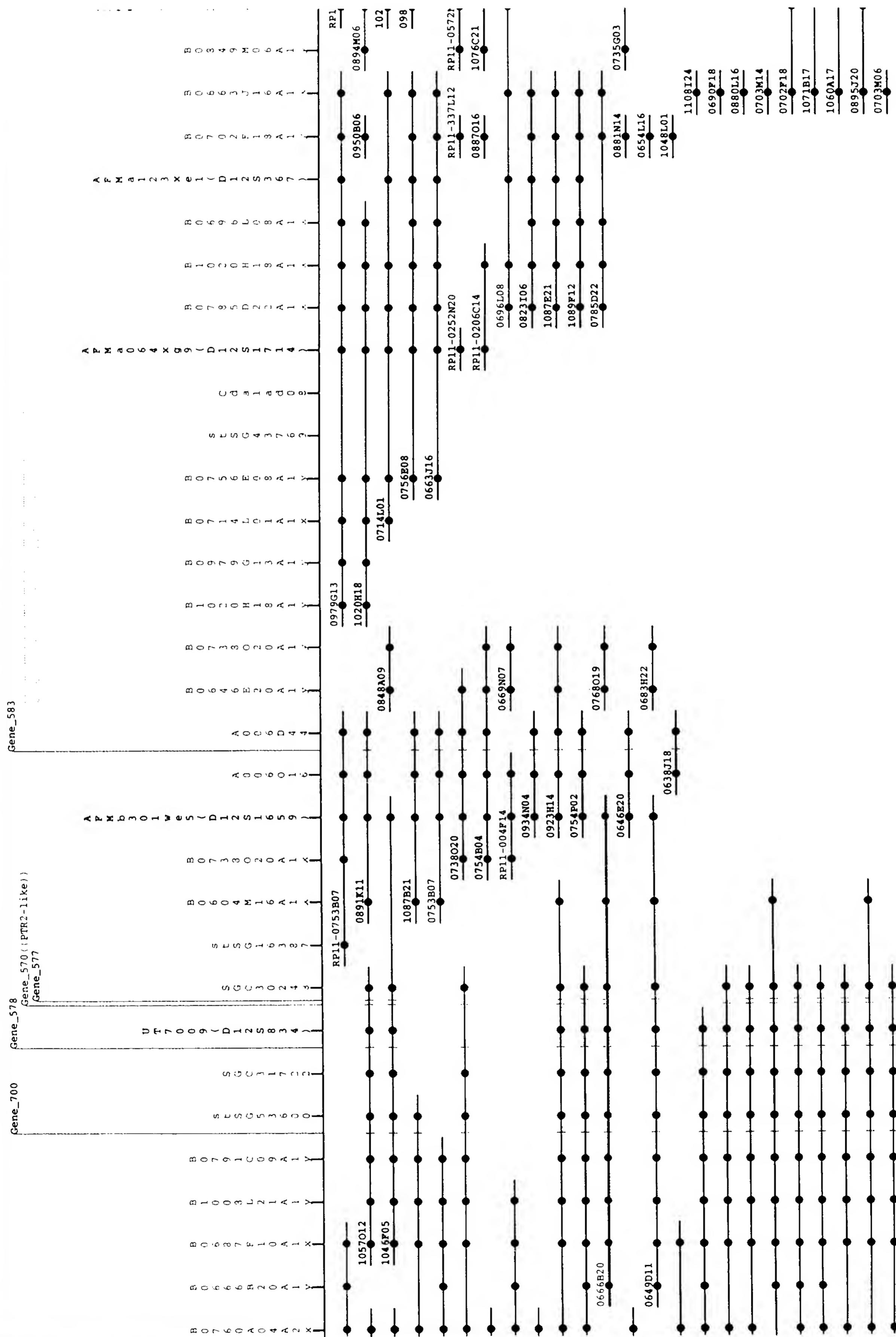
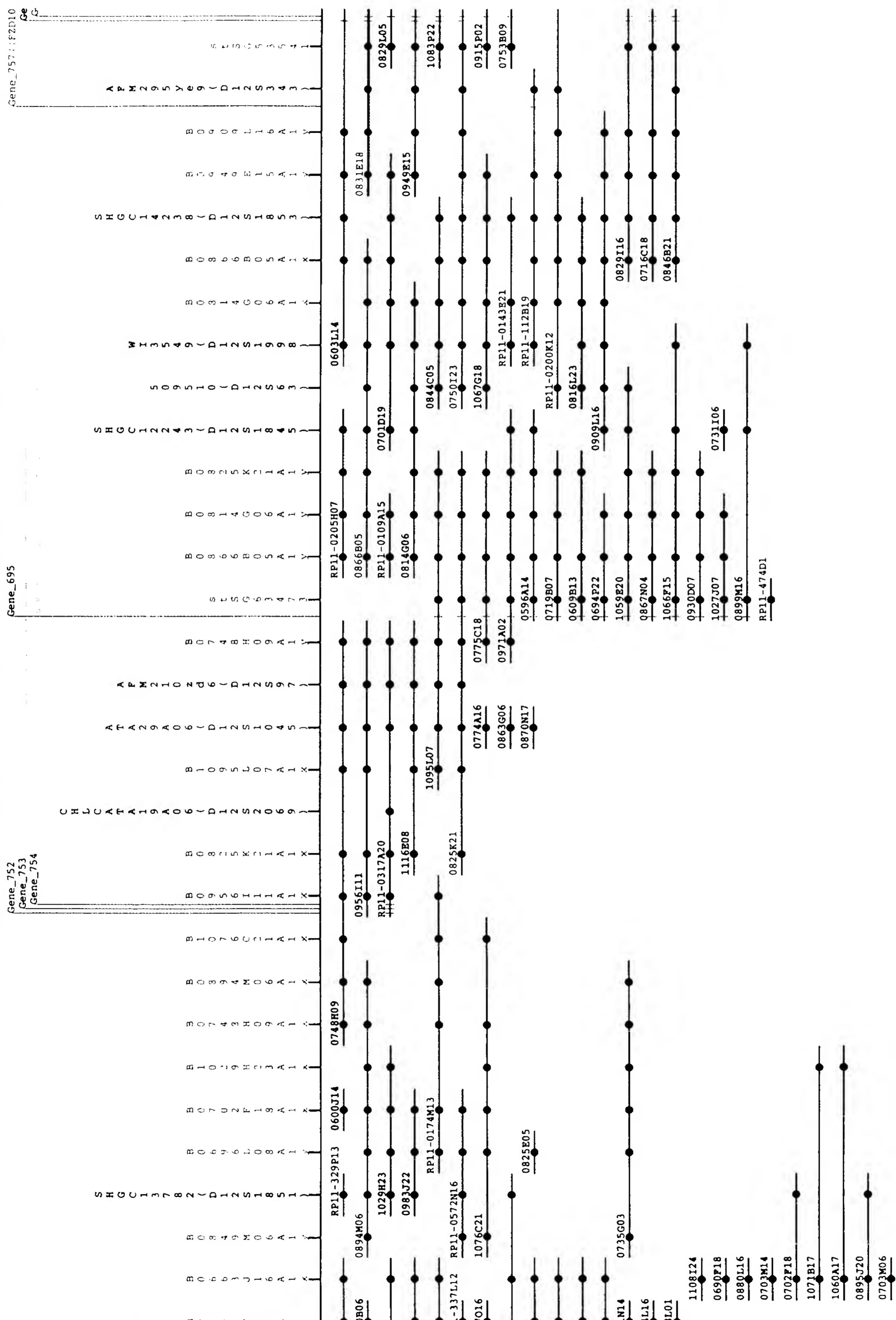
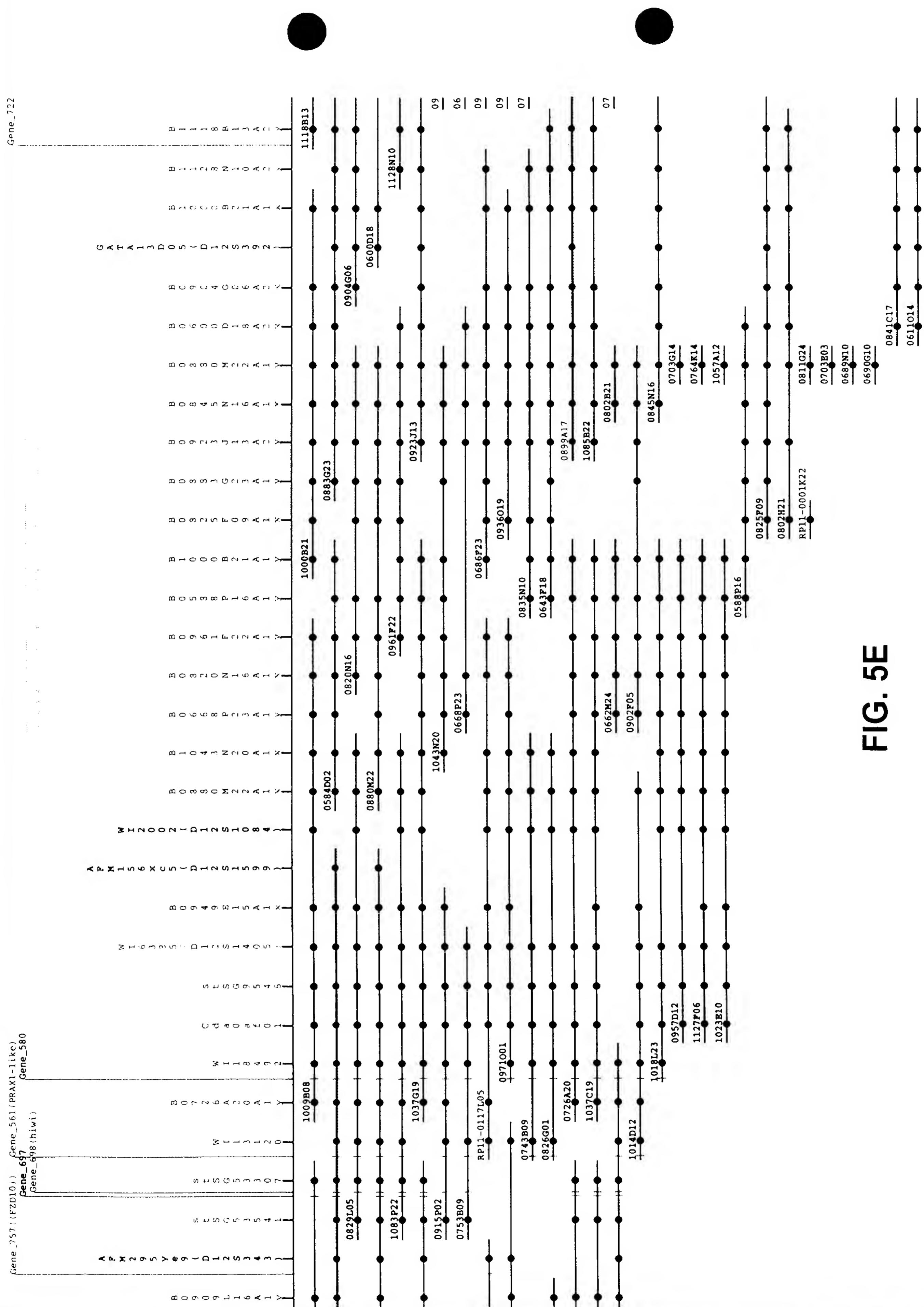


FIG. 5C

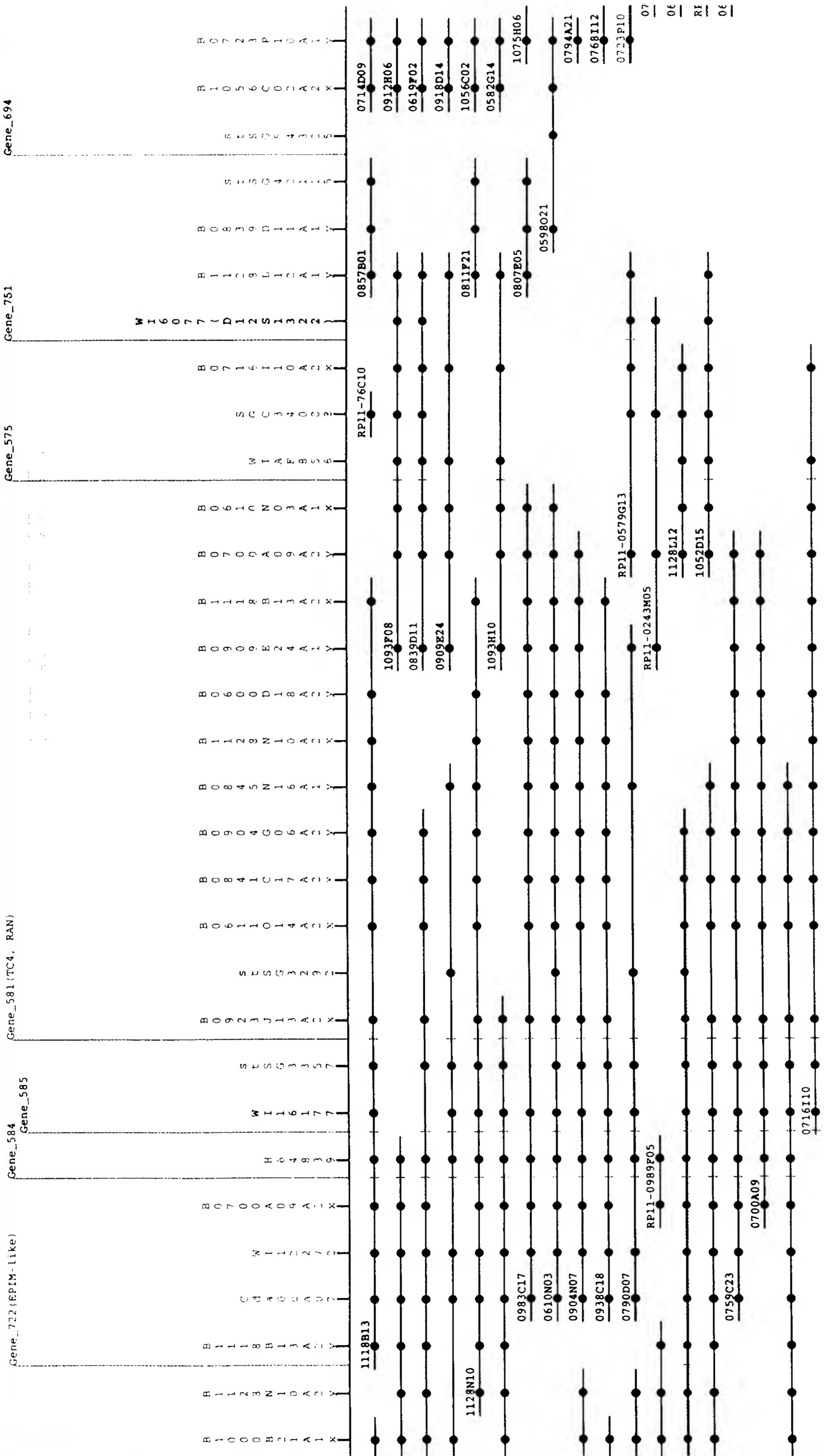


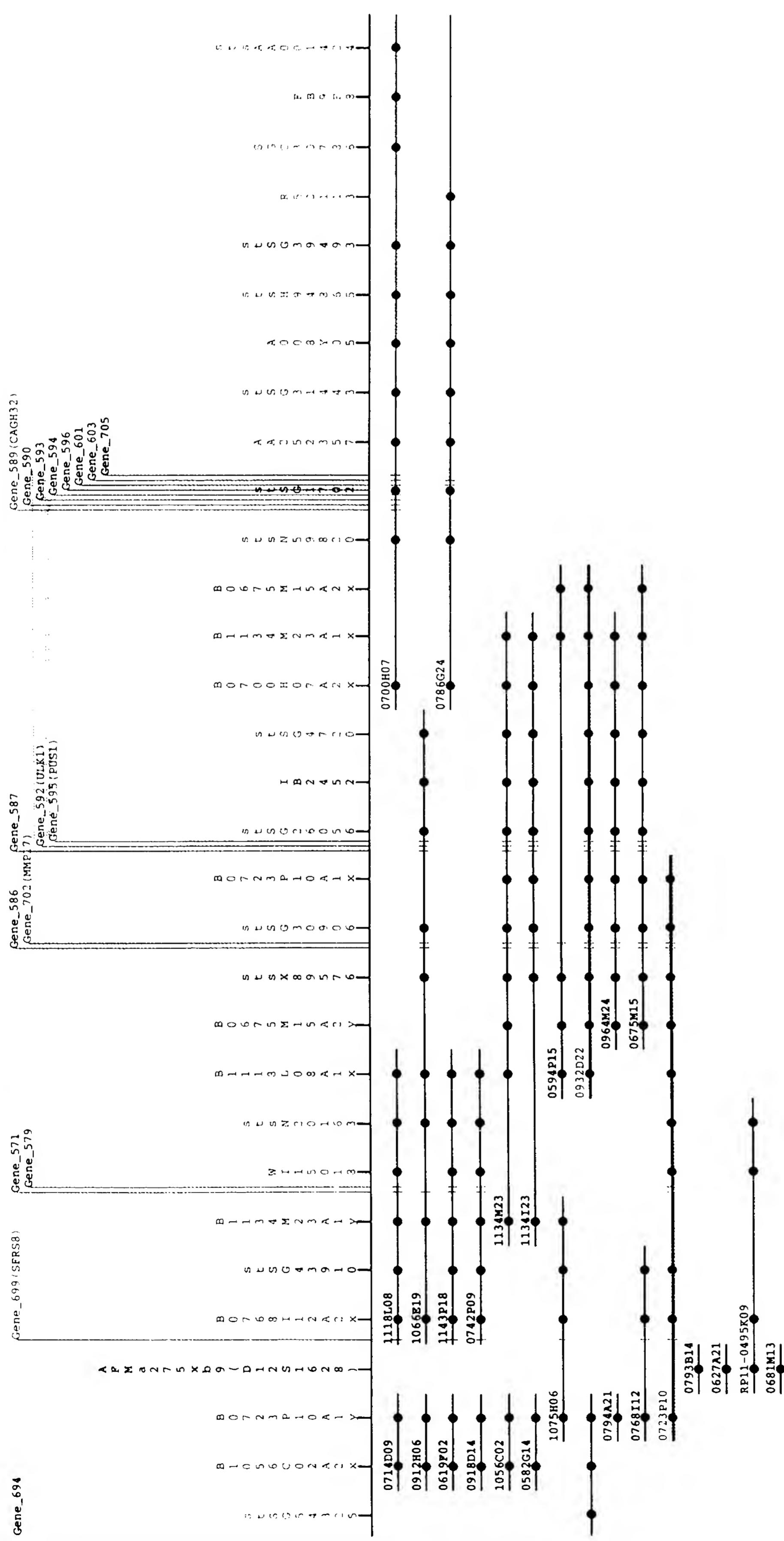
**FIG. 5D**

**FIG. 5E**

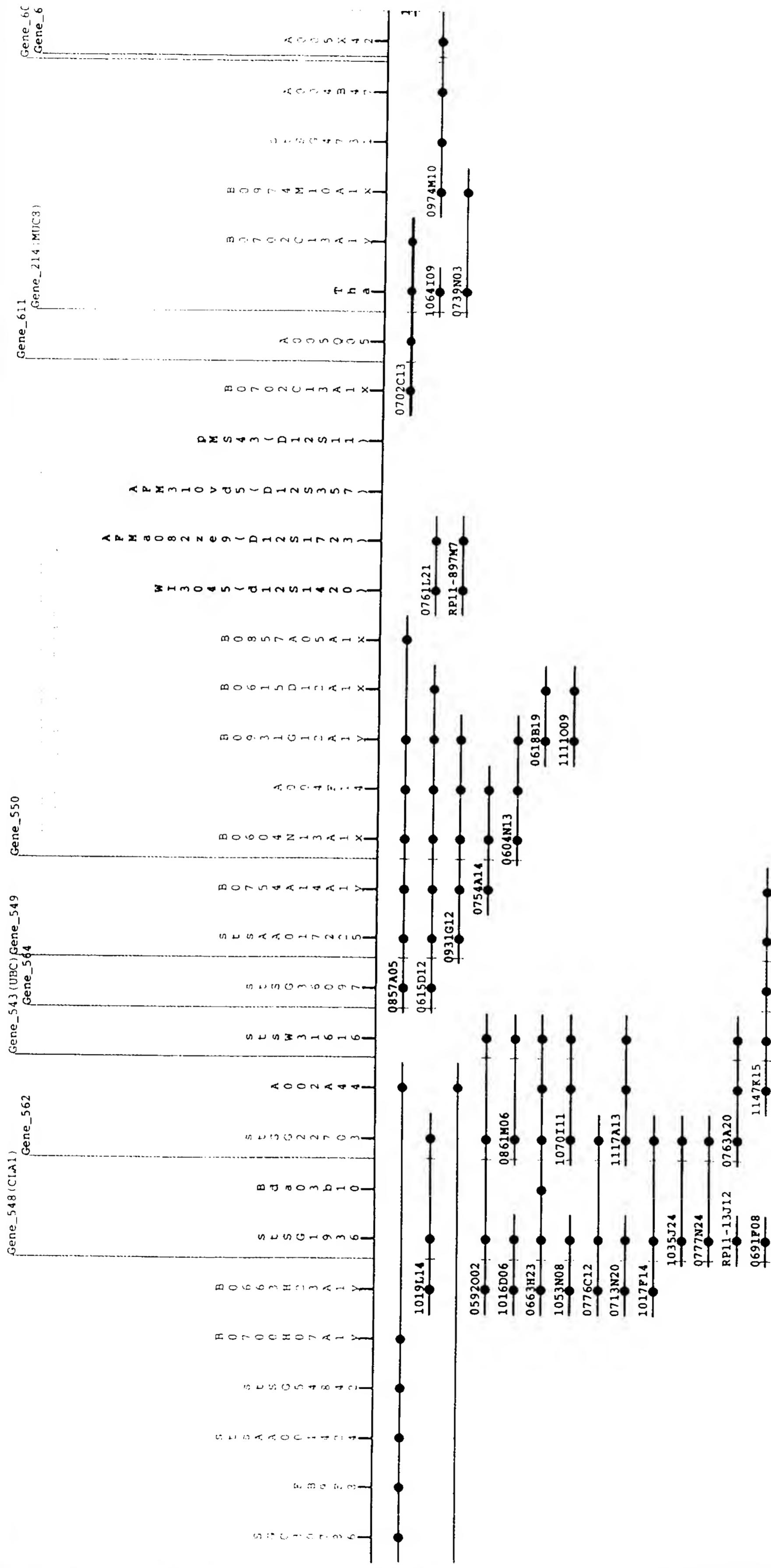


**FIG. 5F**



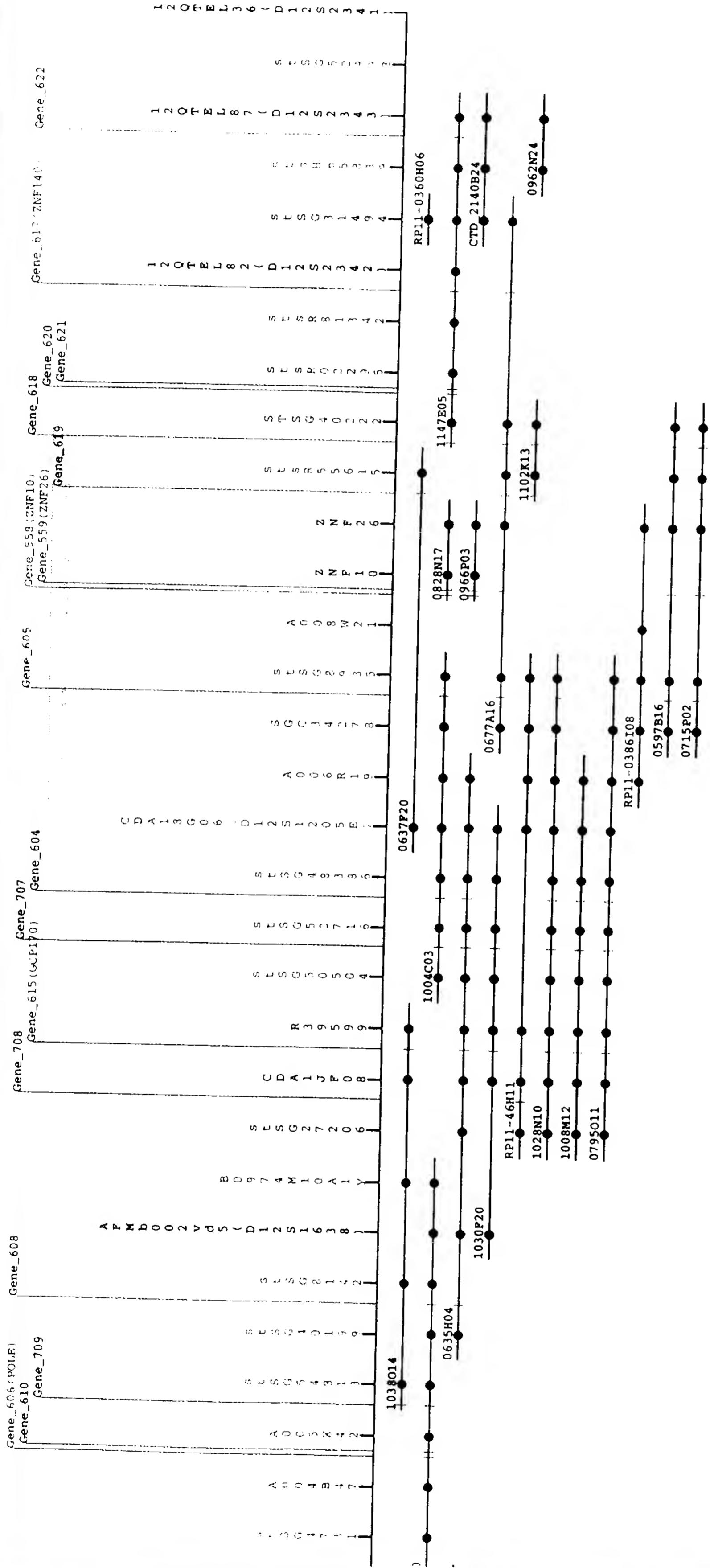


**FIG. 5G**

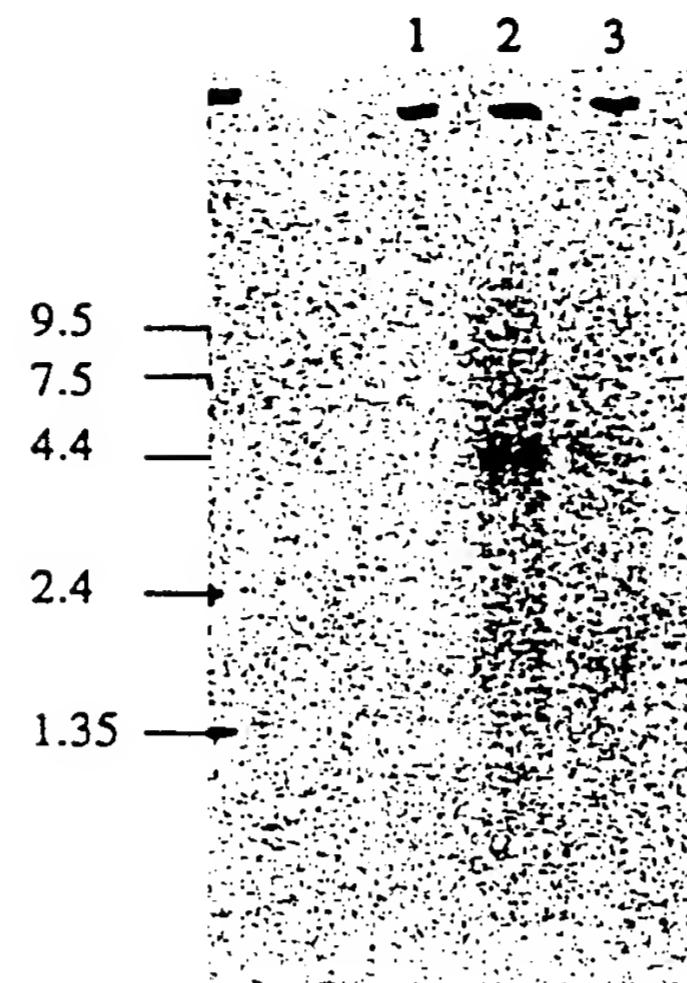


## FIG. 5H

**FIG. 5I**

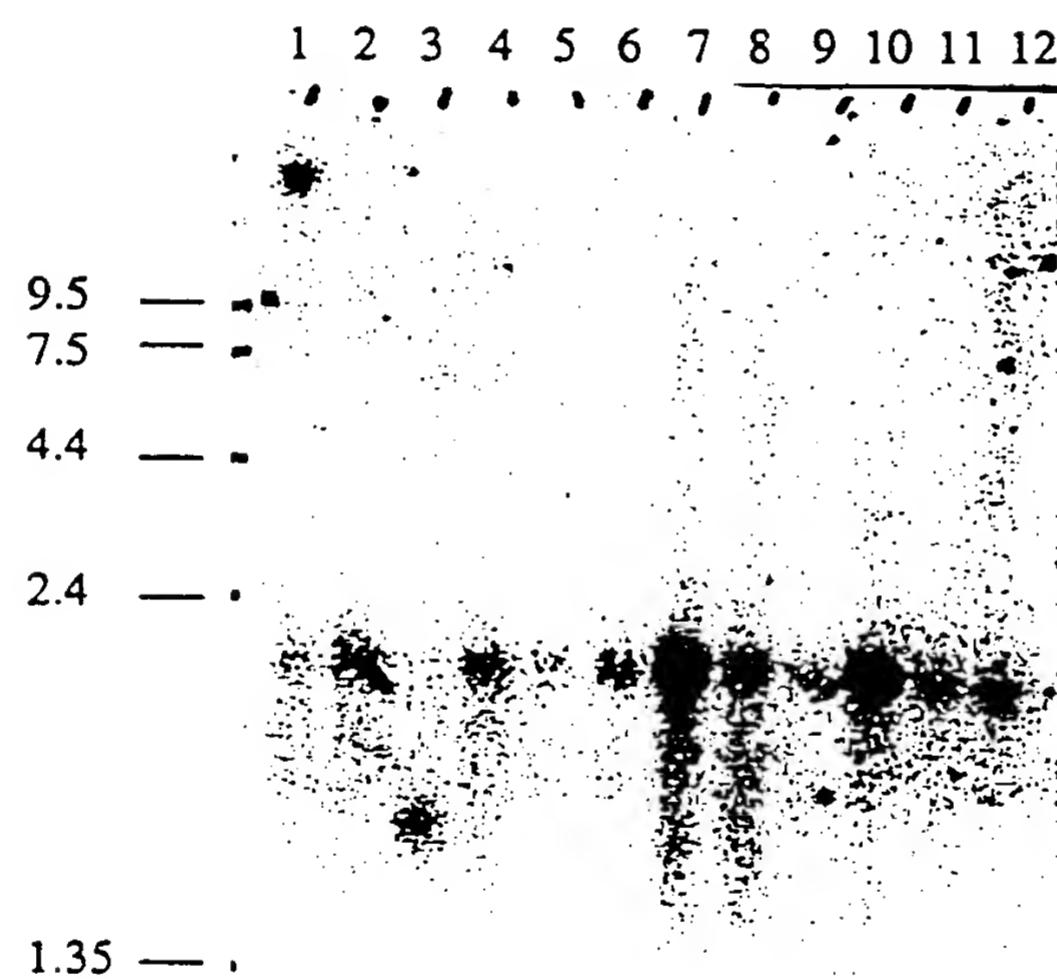


### Gene 214



- 1. Lymphoblastoid cell line
- 2. Lung
- 3. Trachea

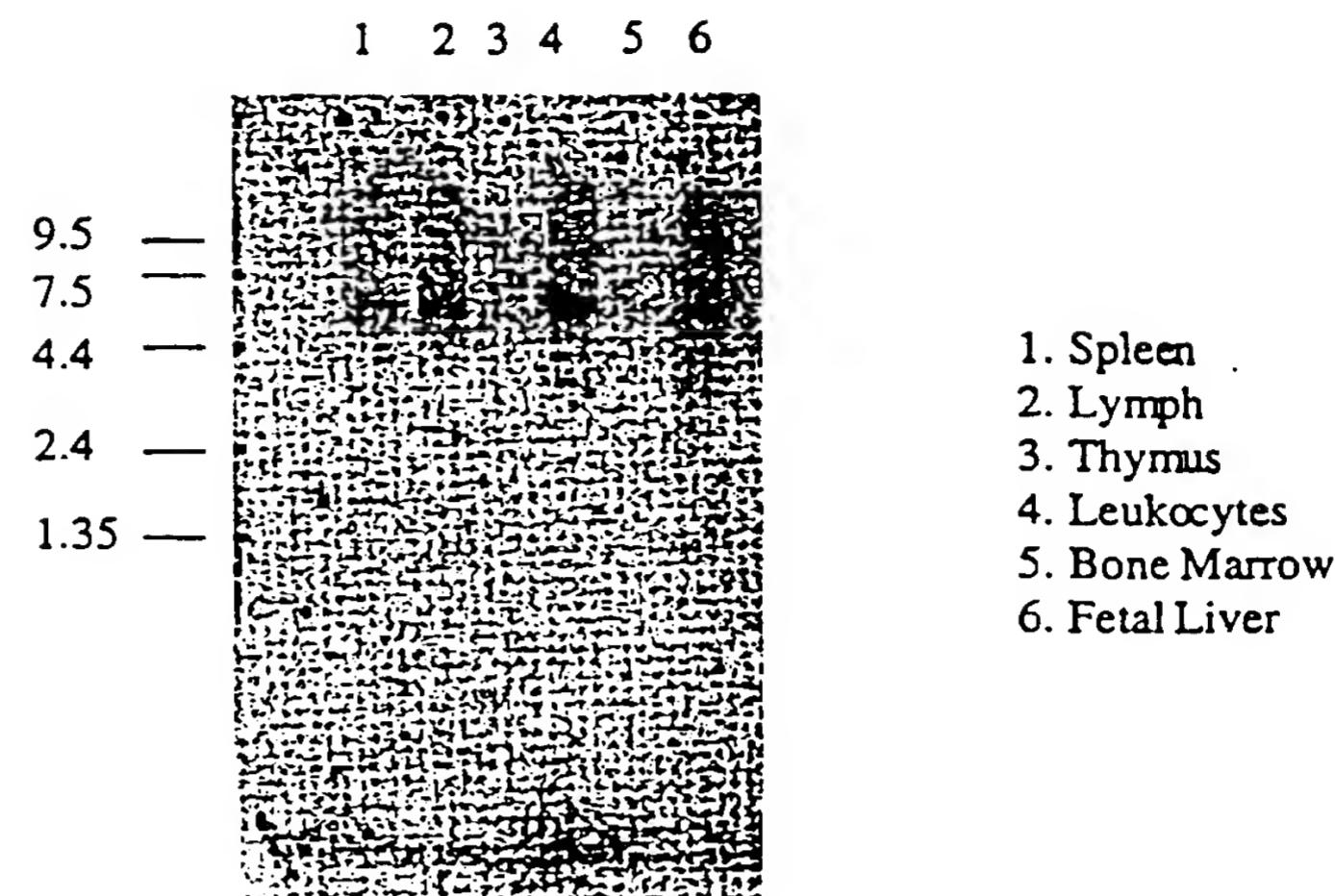
### Gene 436



- 1. Brain
- 2. Heart
- 3. Skeletal Muscle
- 4. Colon
- 5. Thymus
- 6. Spleen
- 7. Kidney
- 8. Liver
- 9. Small Intestine
- 10. Placenta
- 11. Lung
- 12. Leukocytes

FIG. 6 A

## Gene 454



## Gene 515

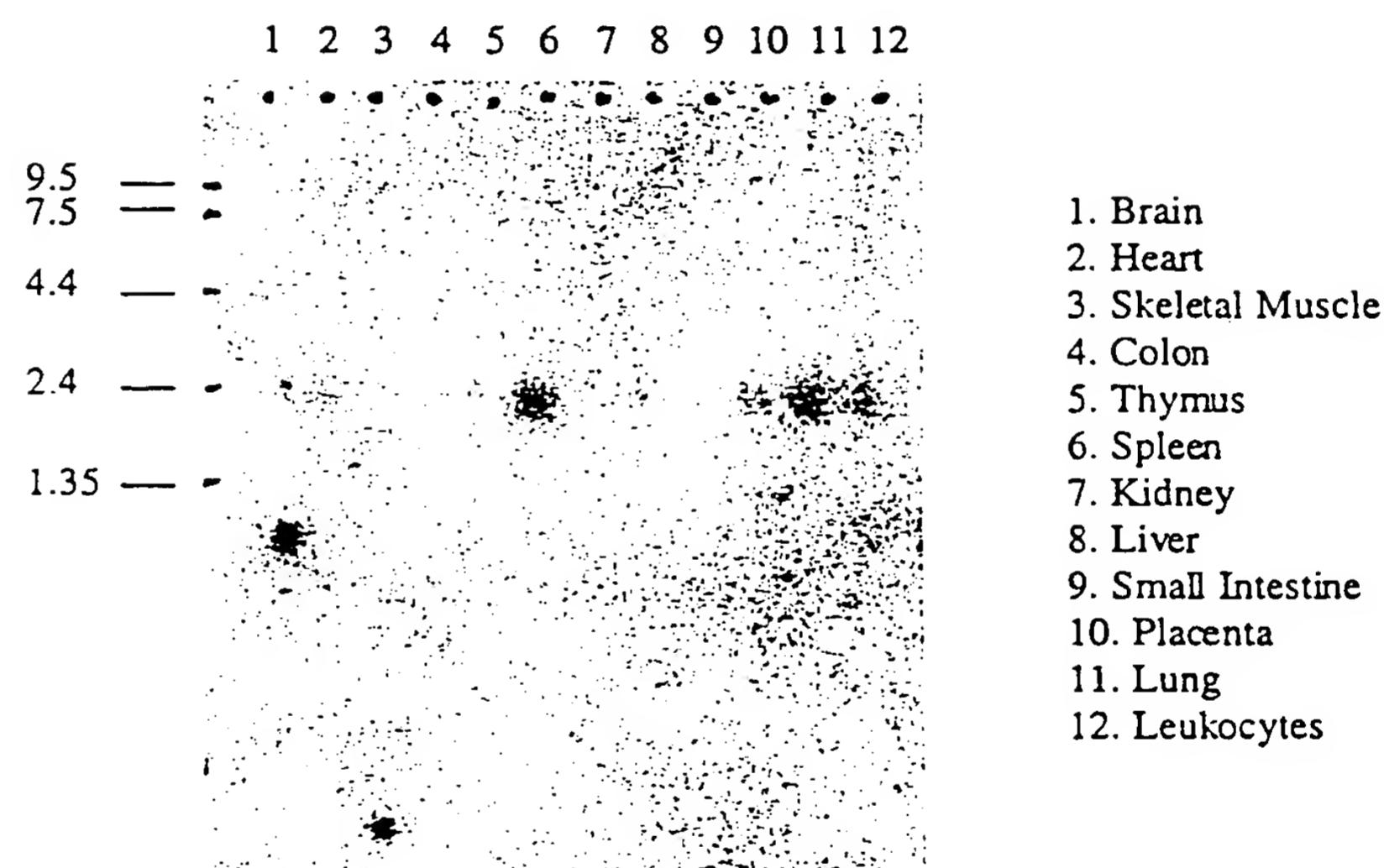
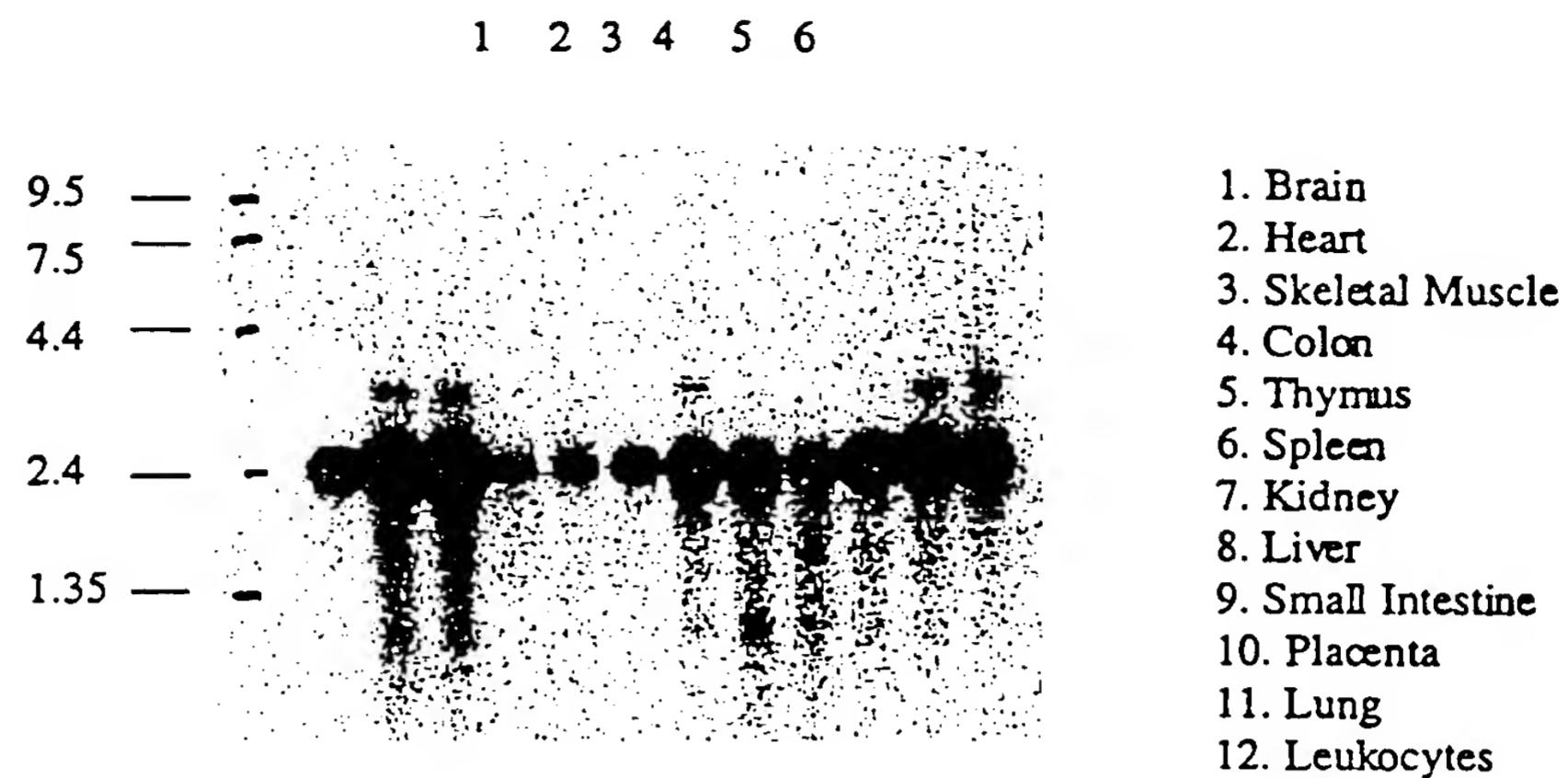
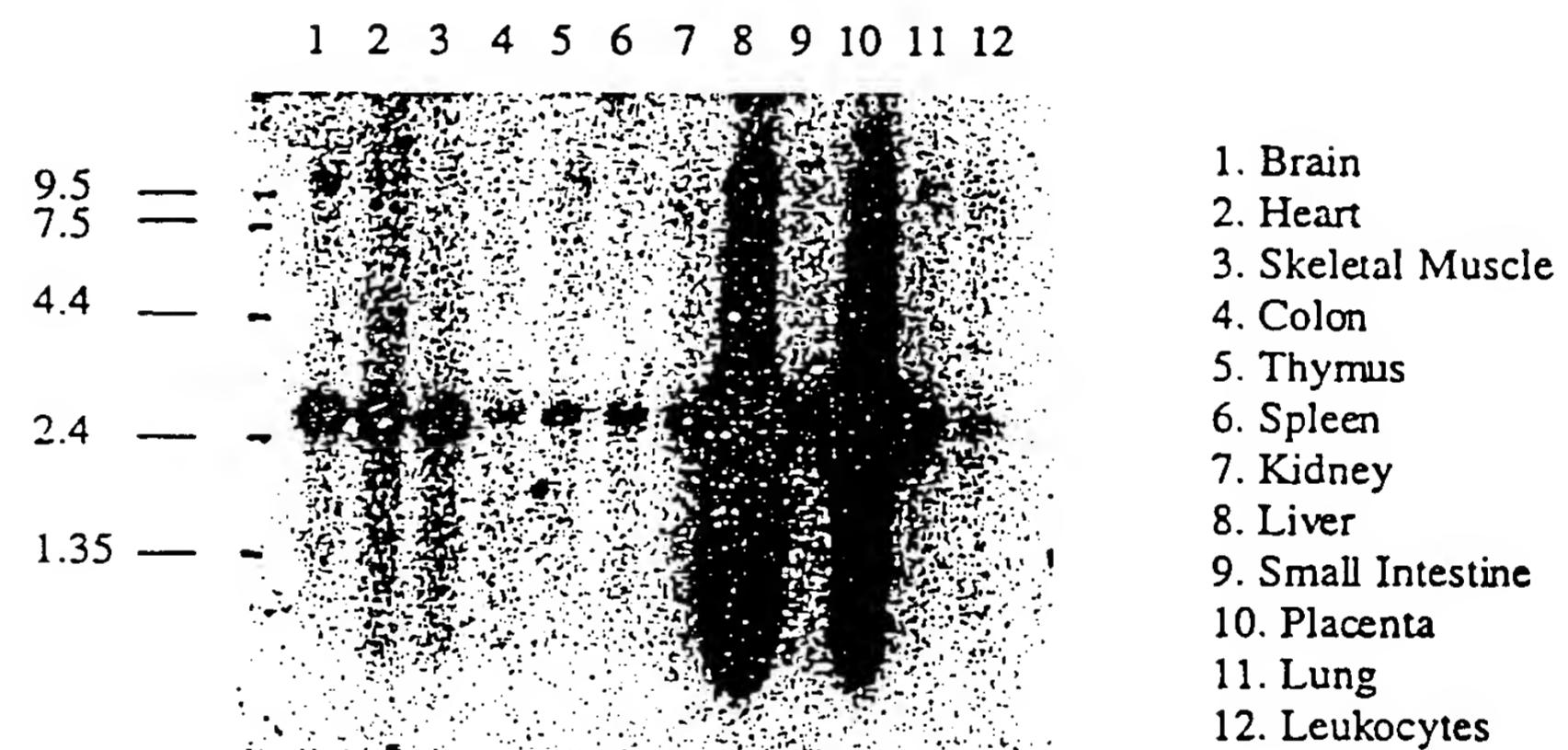


FIG. 6 B

### Gene 543

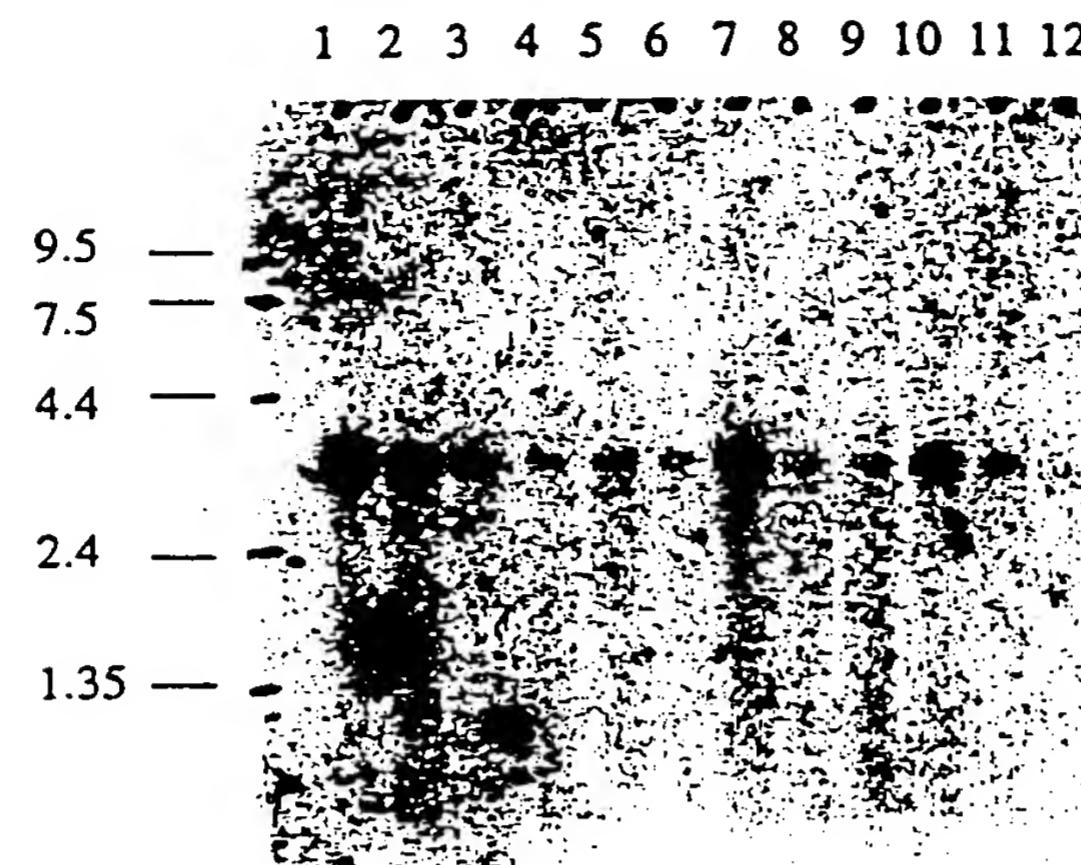


### Gene 548



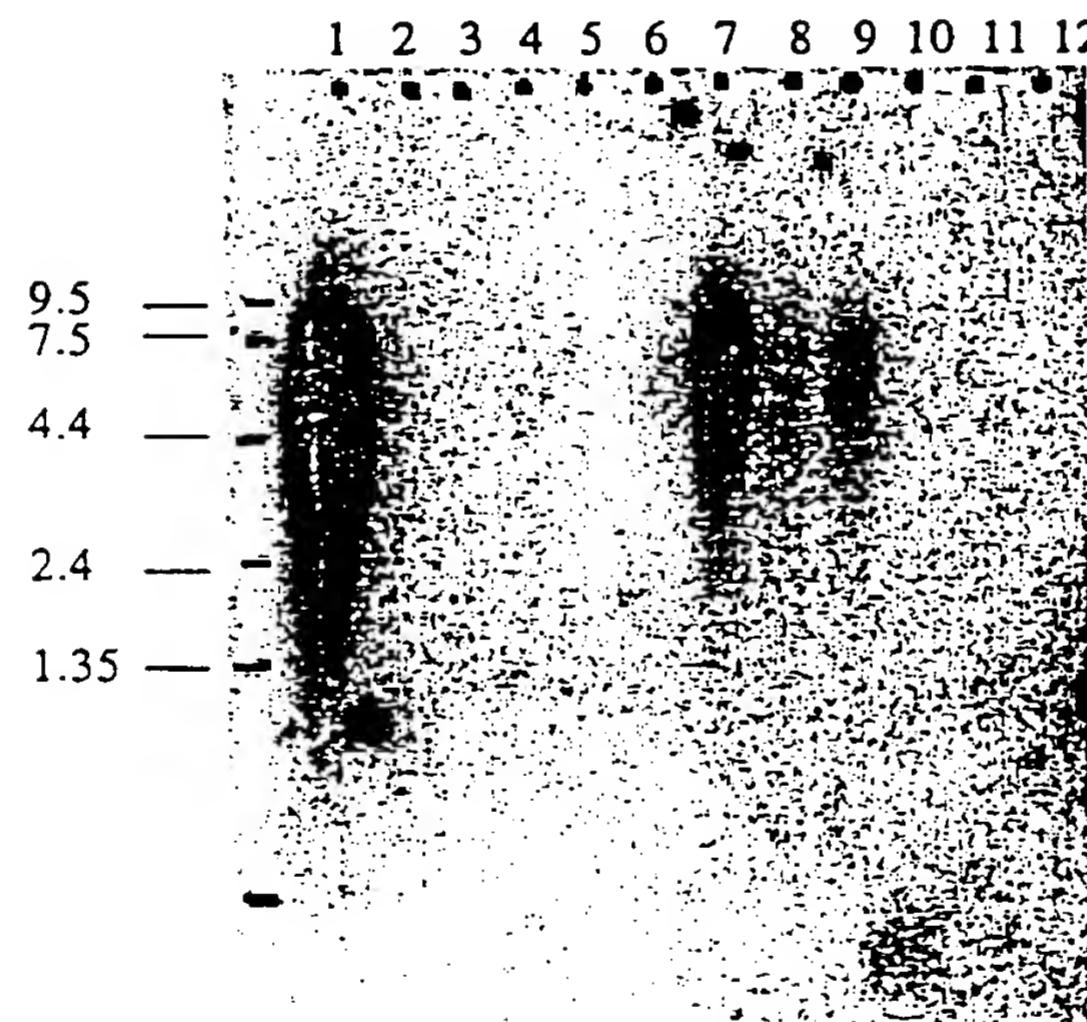
**FIG. 6 C**

## Gene 550



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

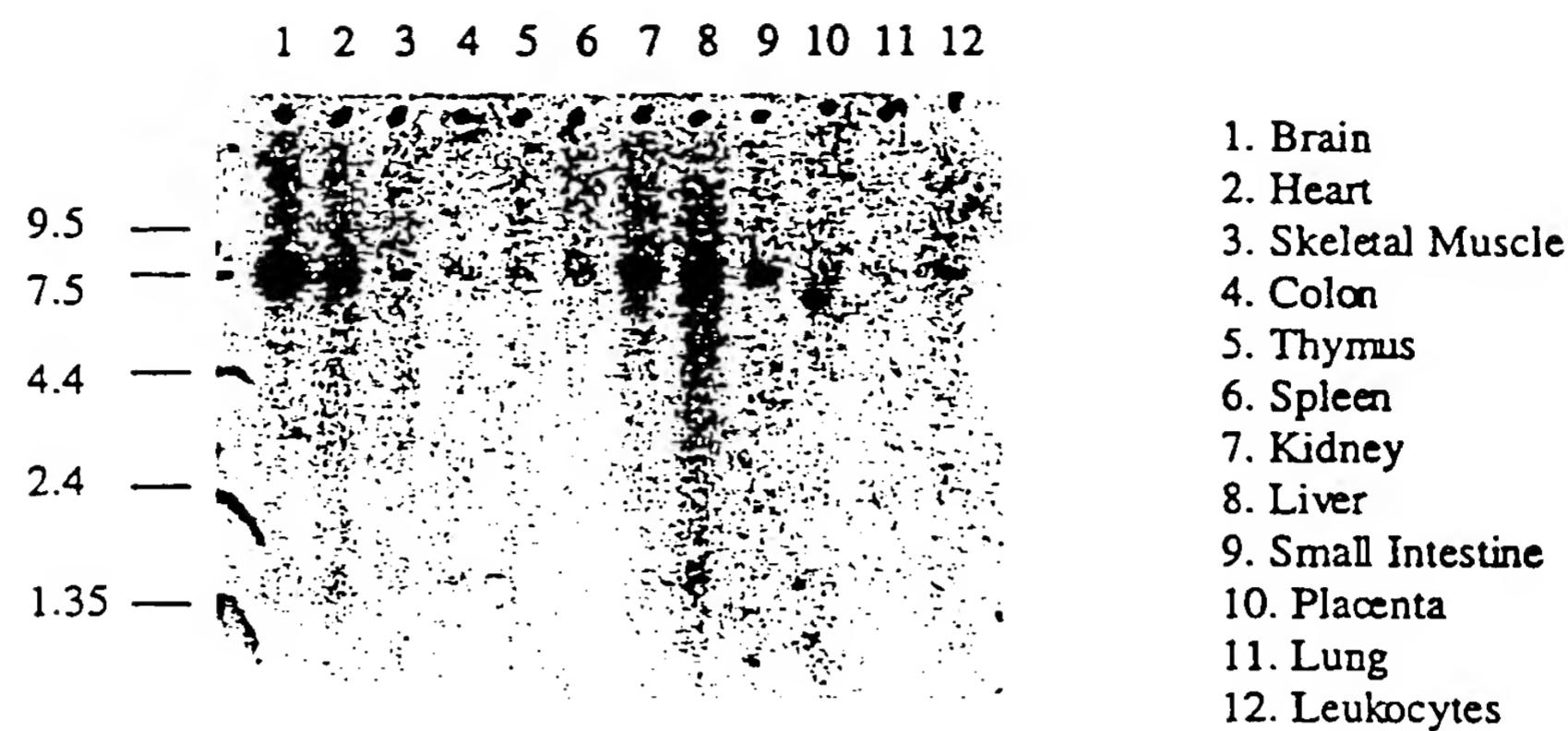
## Gene 561



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 D

### Gene 564



### Gene 570

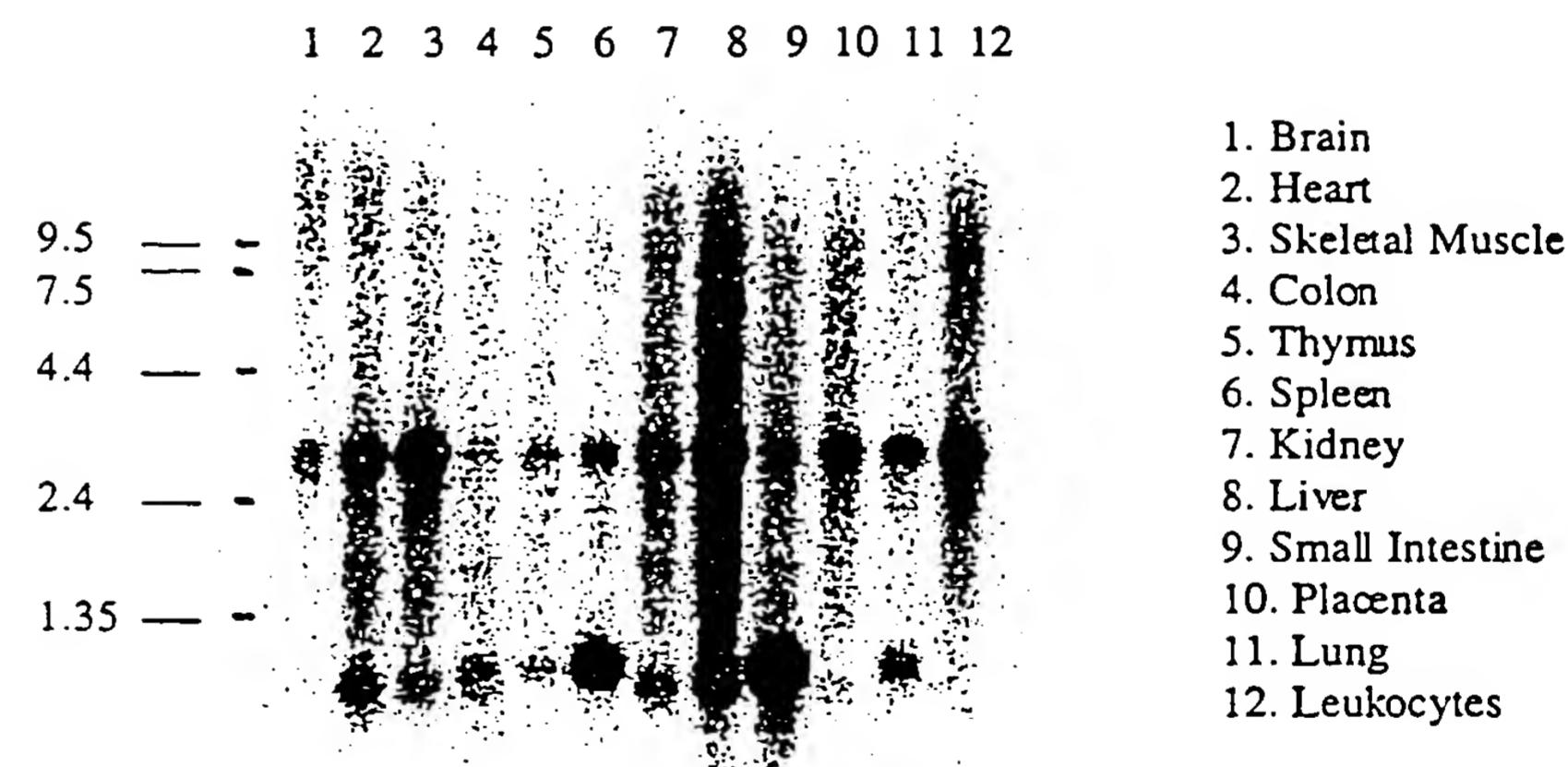
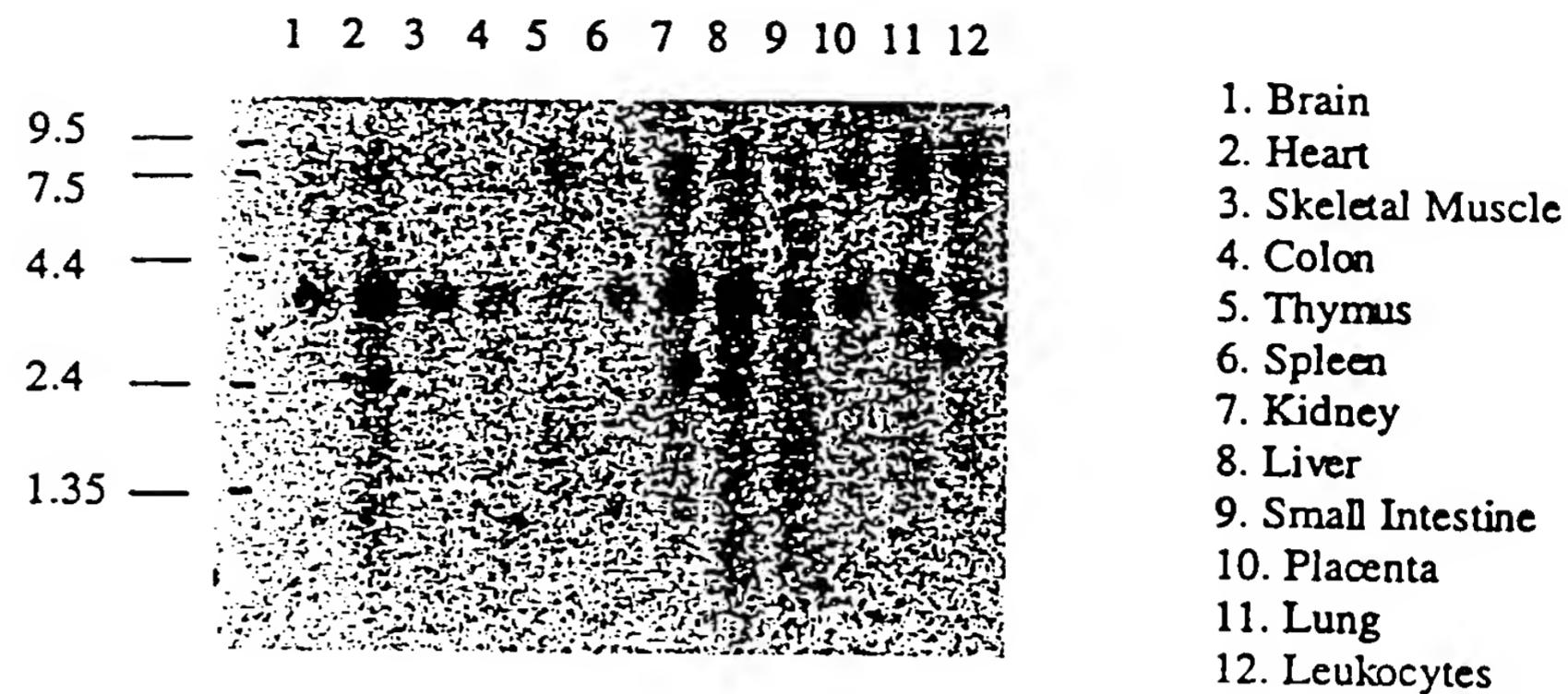


FIG. 6 E

## Gene 576



## Gene 577

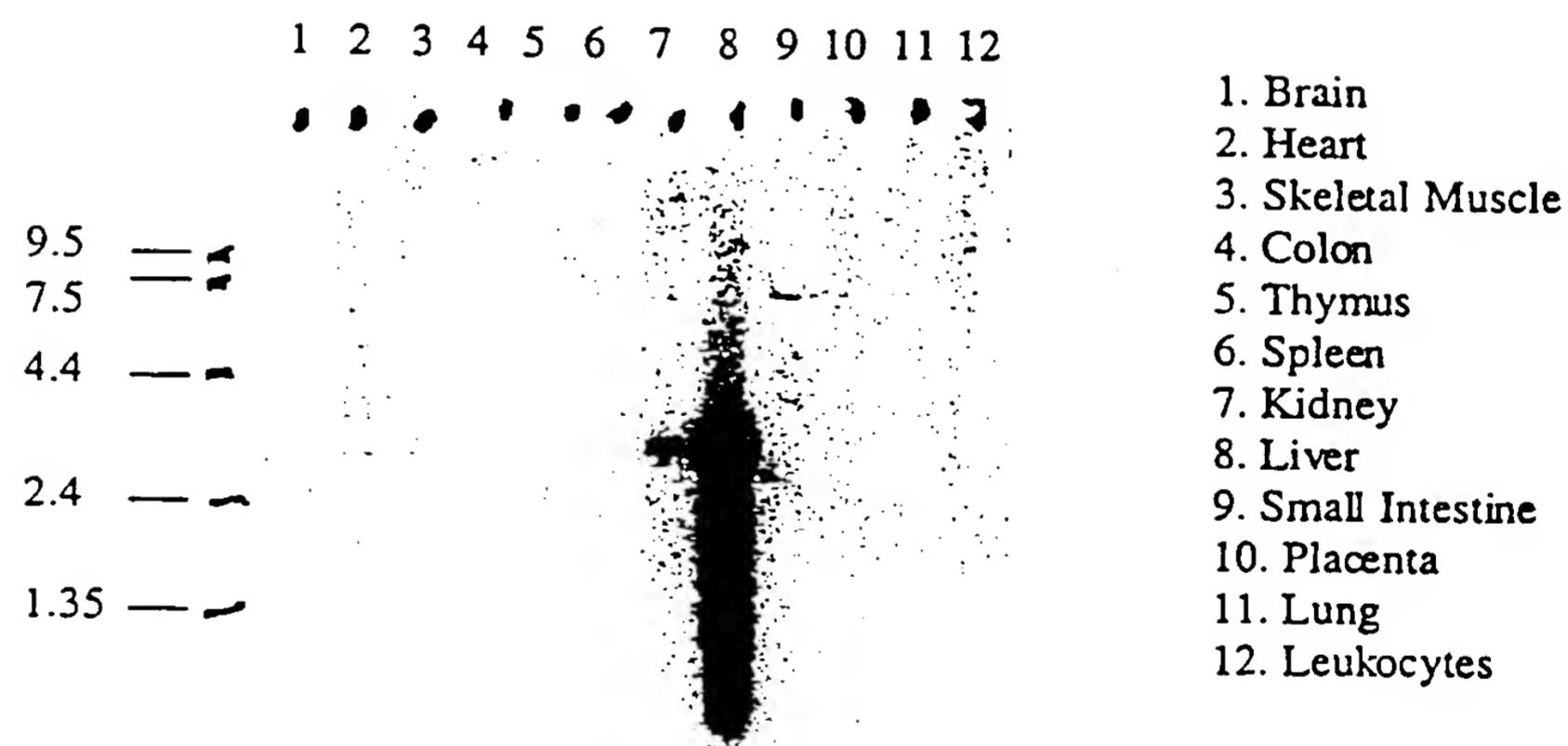
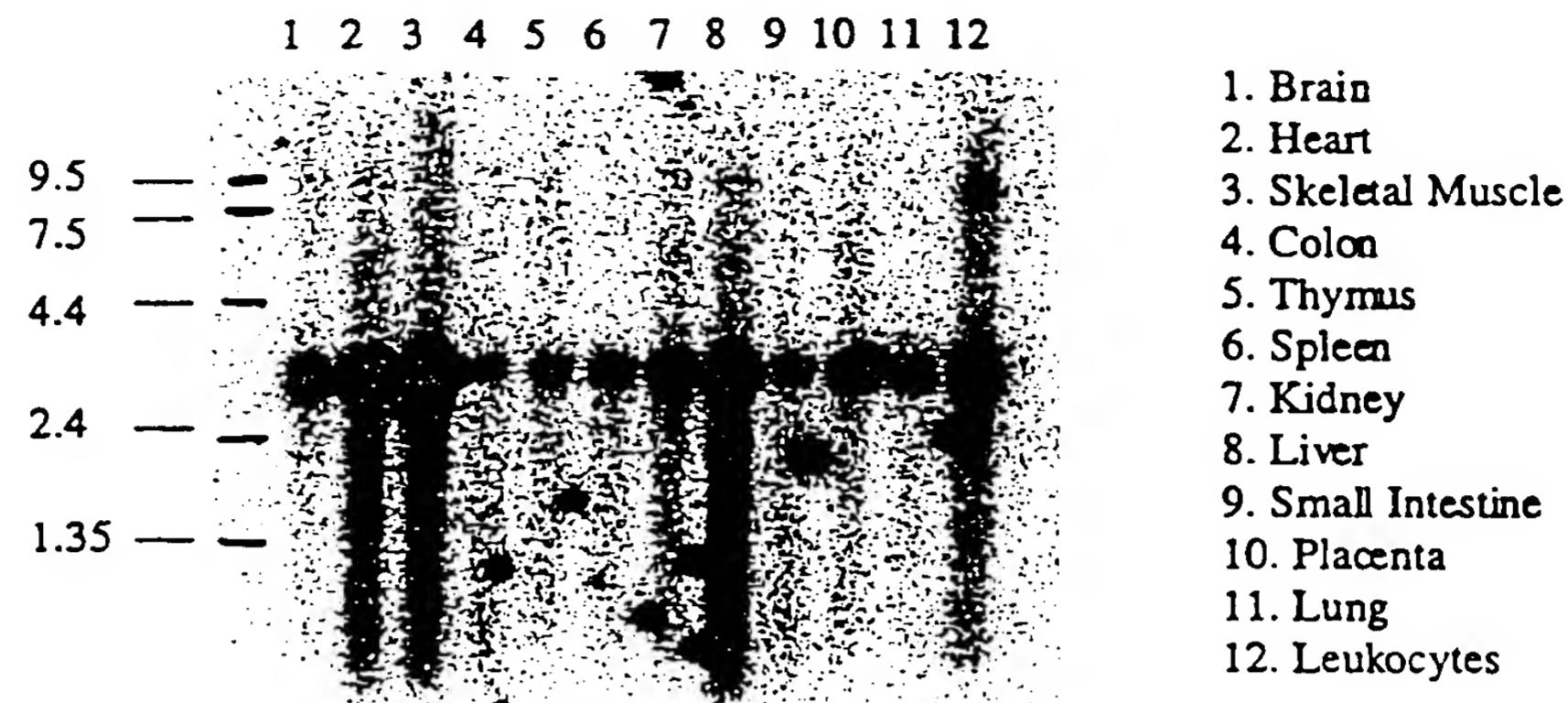


FIG. 6 F

### Gene 578



### Gene 579

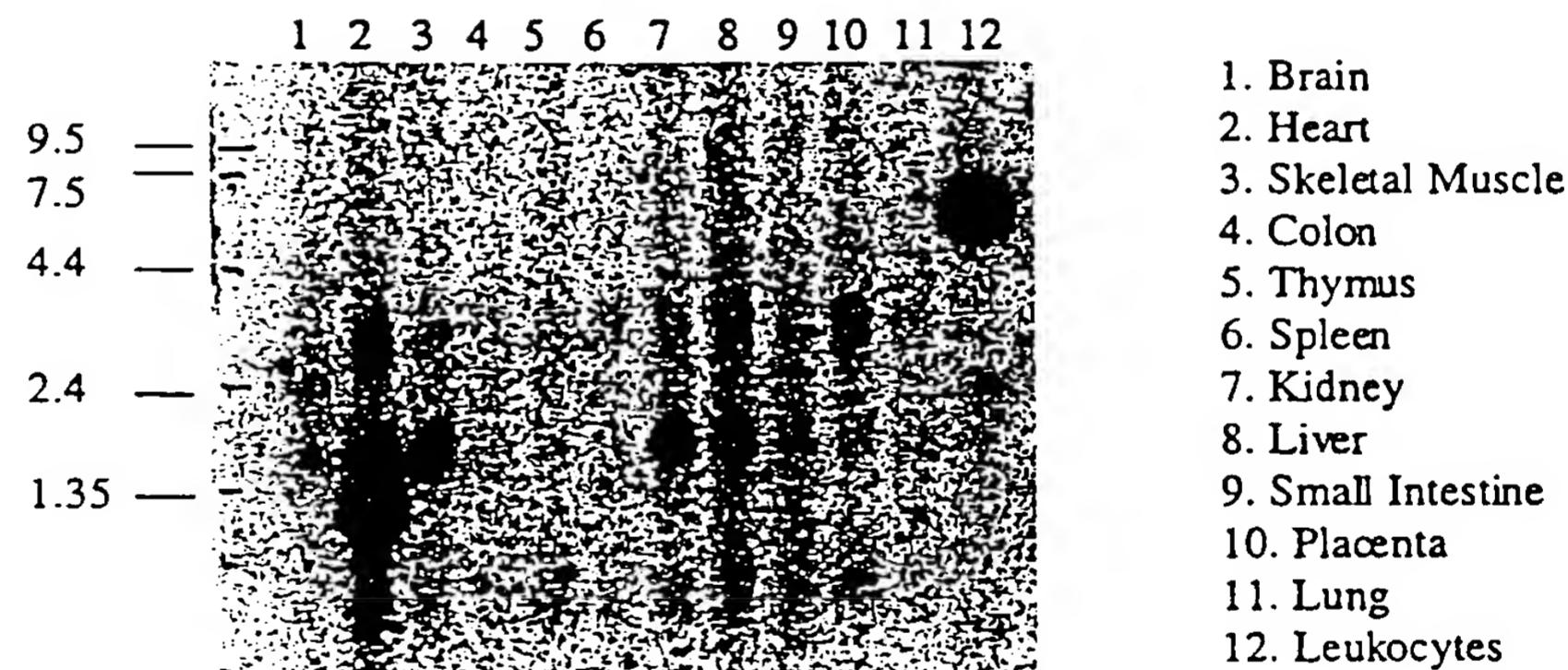
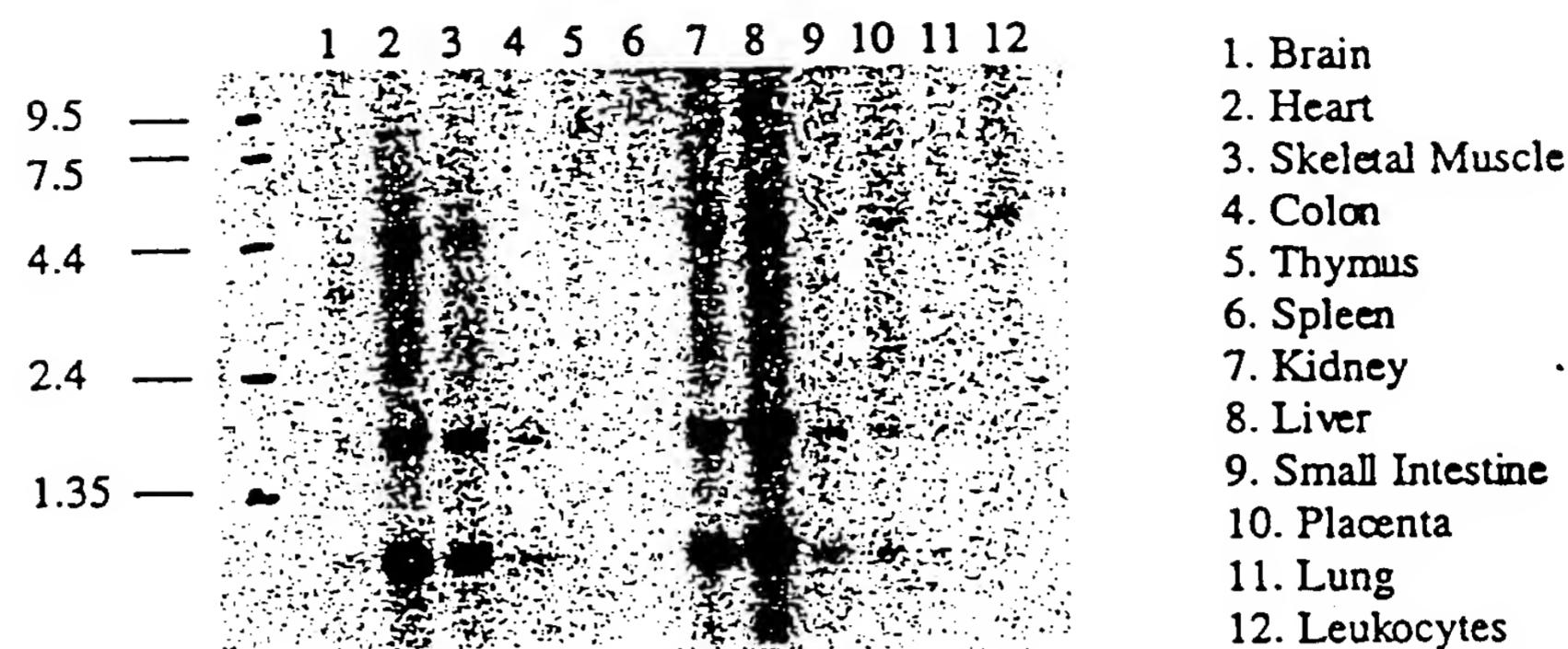


FIG. 6 G

## Gene 580



## Gene 581

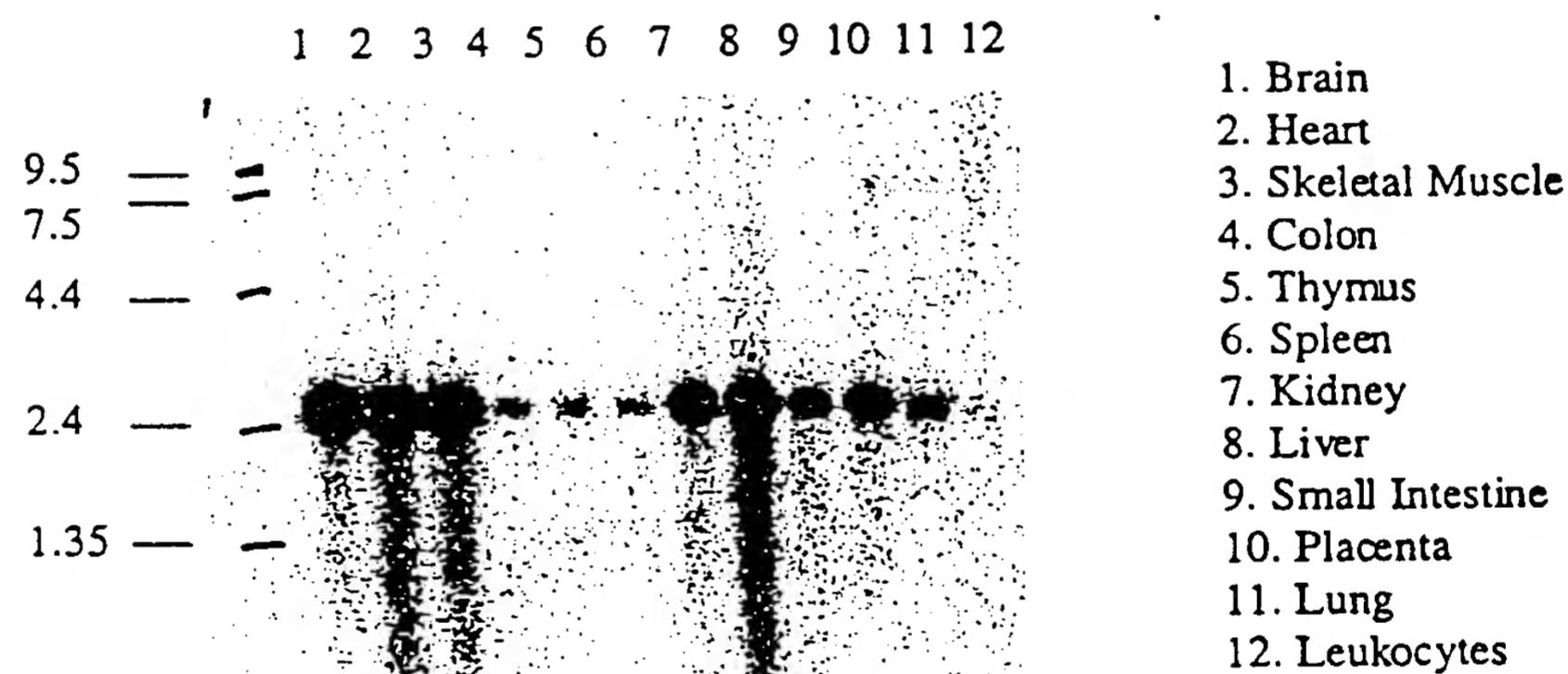
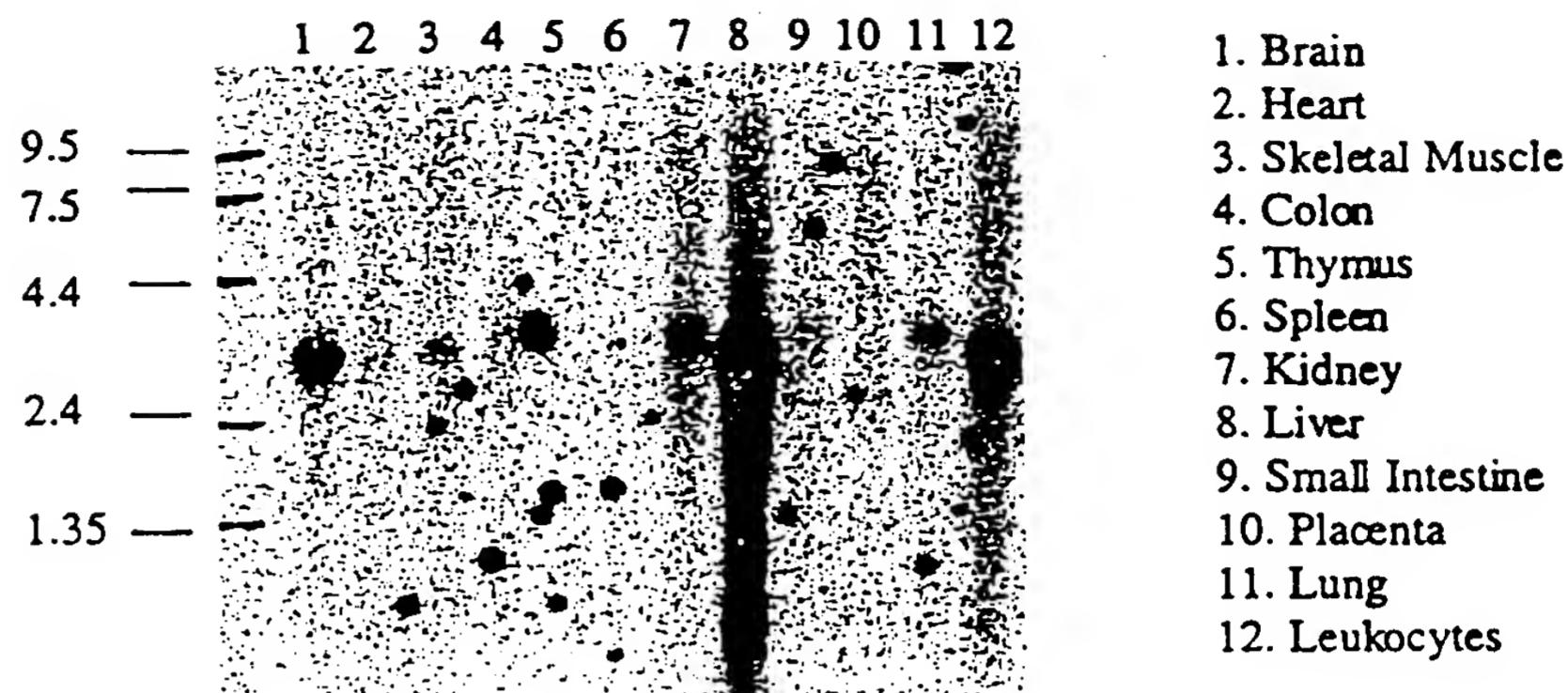


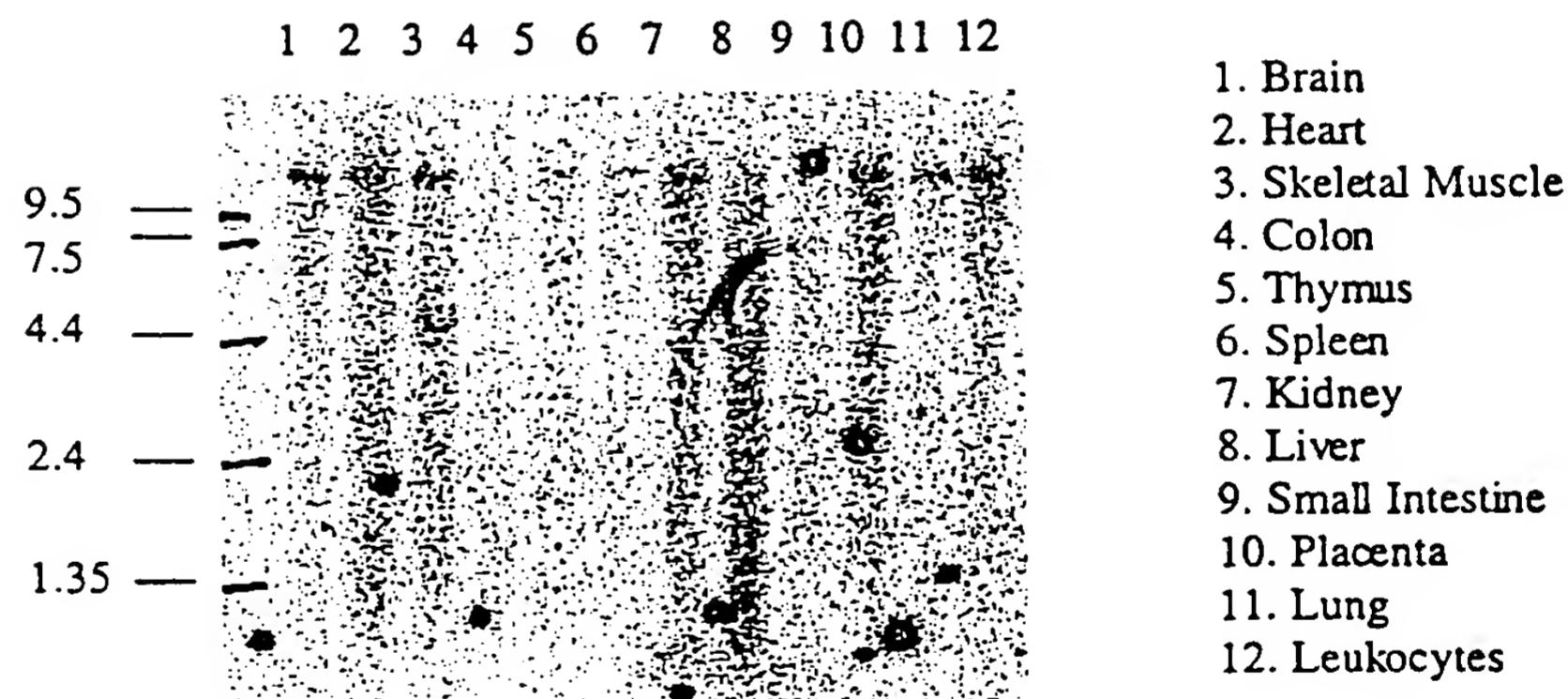
FIG. 6 H

### Gene 583



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

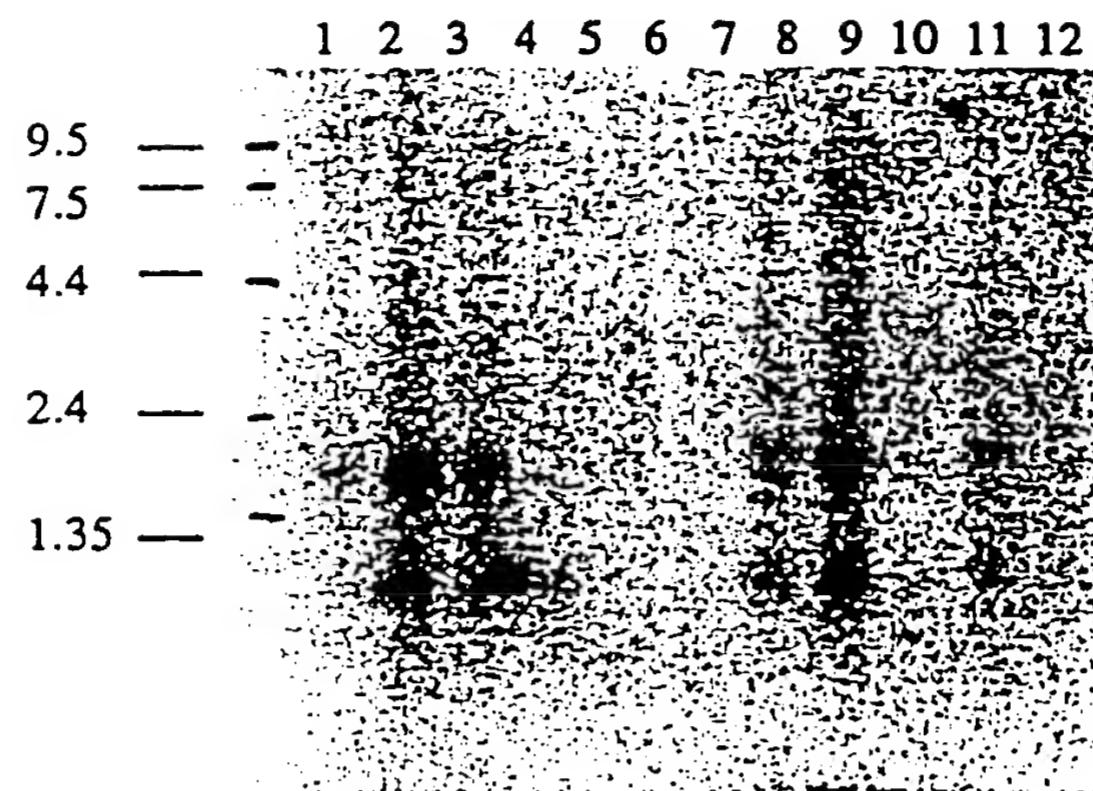
### Gene 589



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

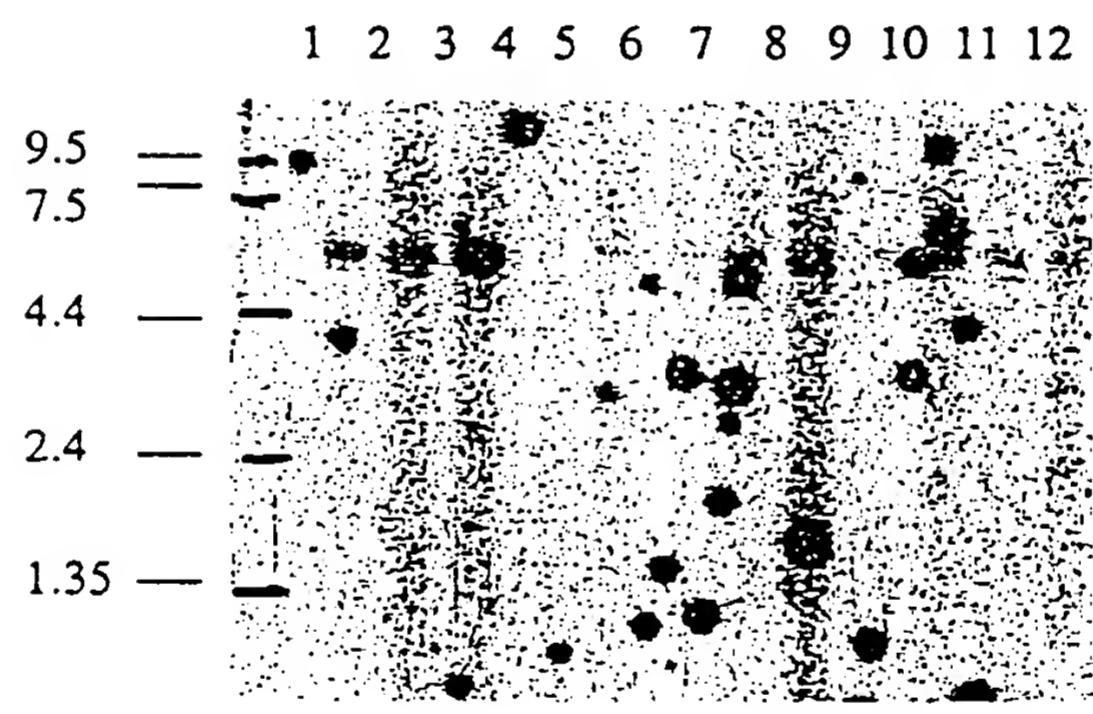
FIG. 6 I

## Gene 590



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

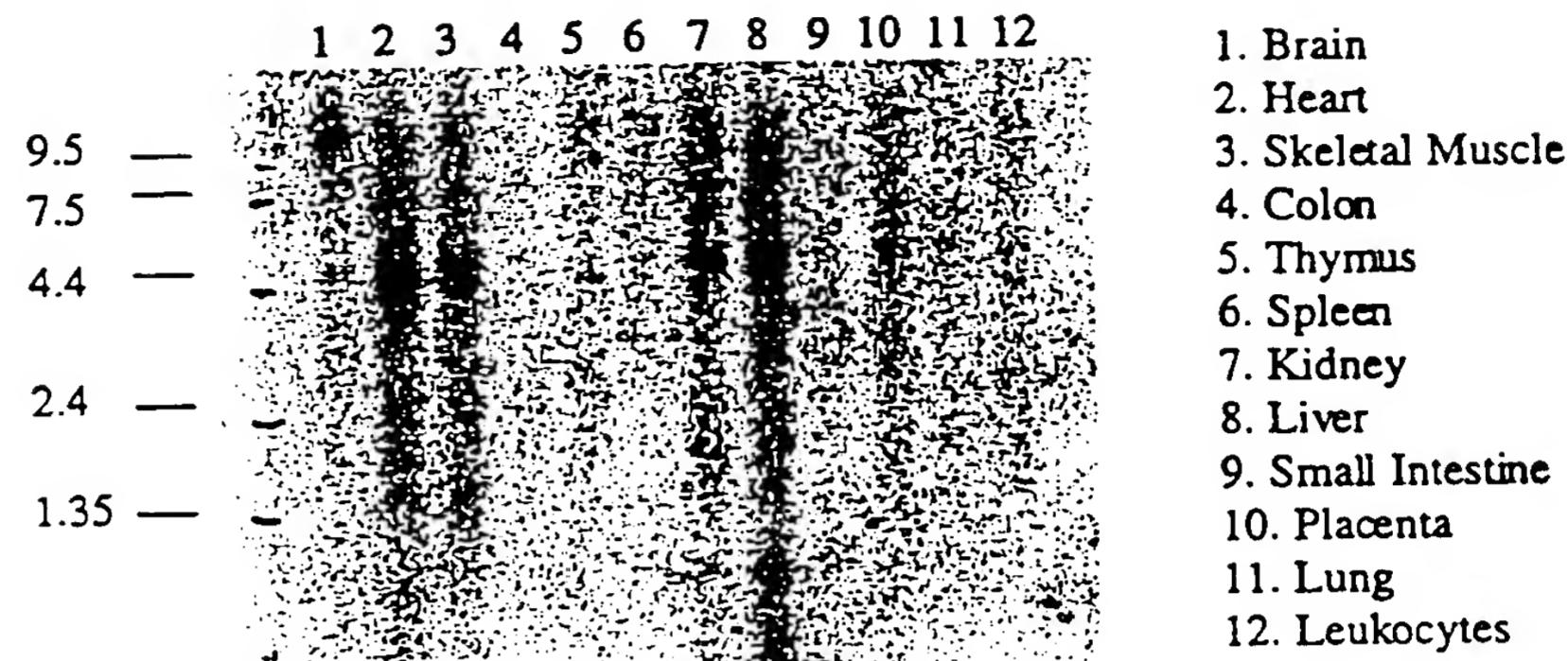
## Gene 592



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 J

### Gene 594



### Gene 595

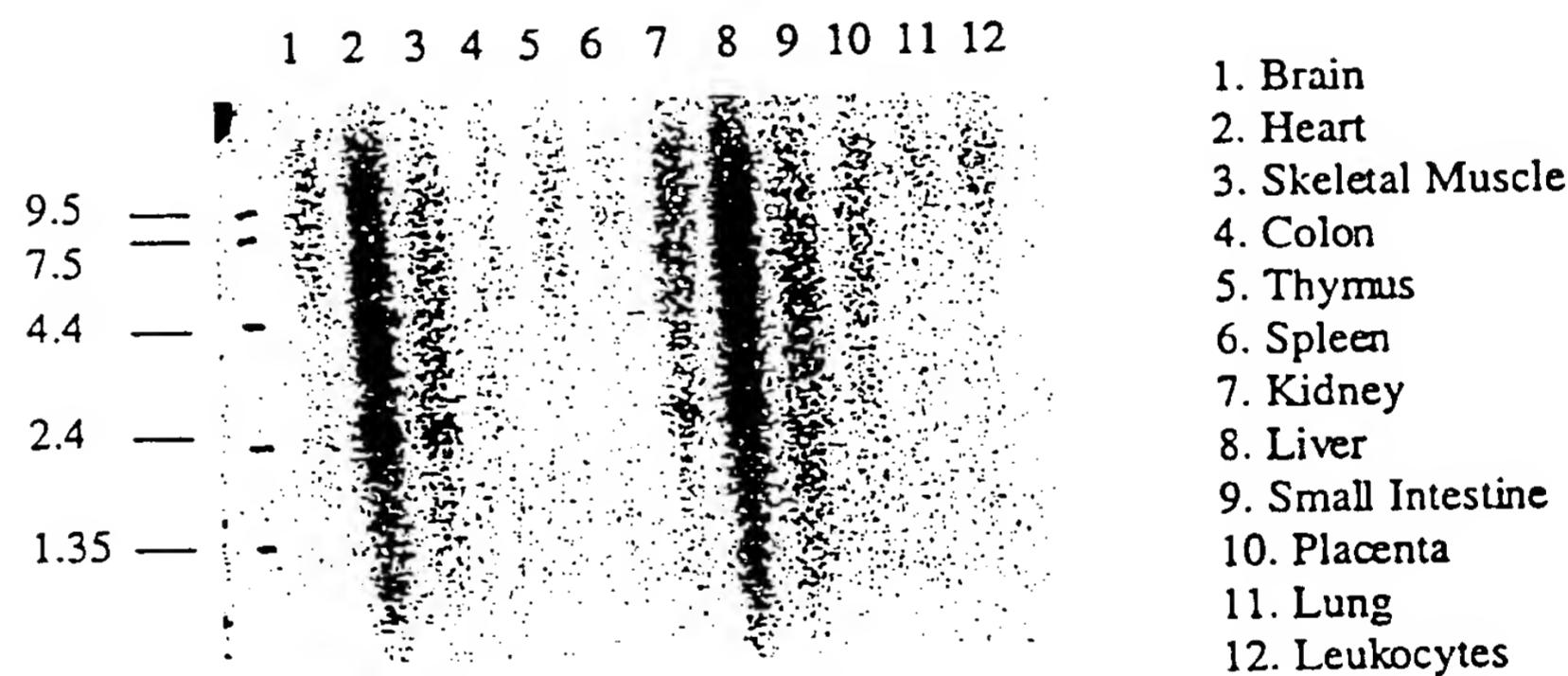
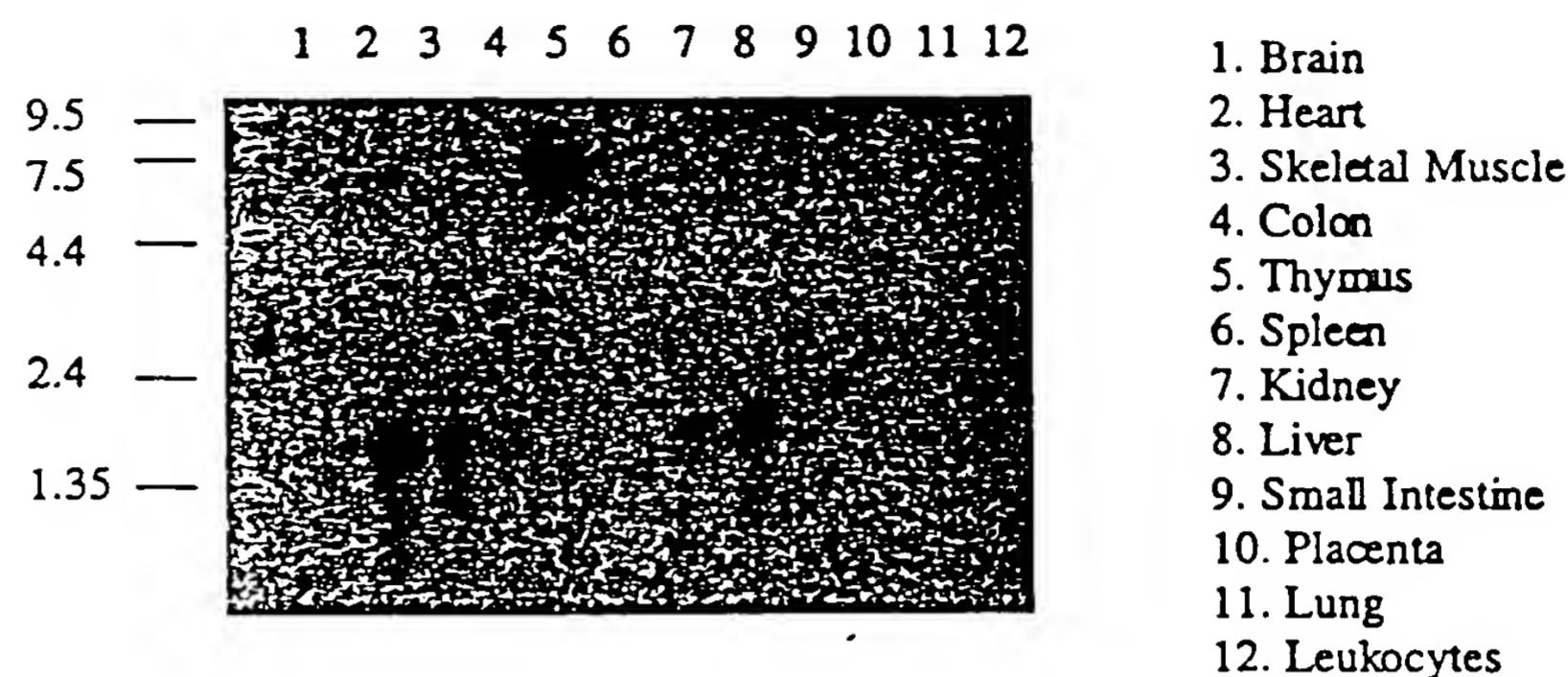


FIG. 6 K

### Gene 596



### Gene 604

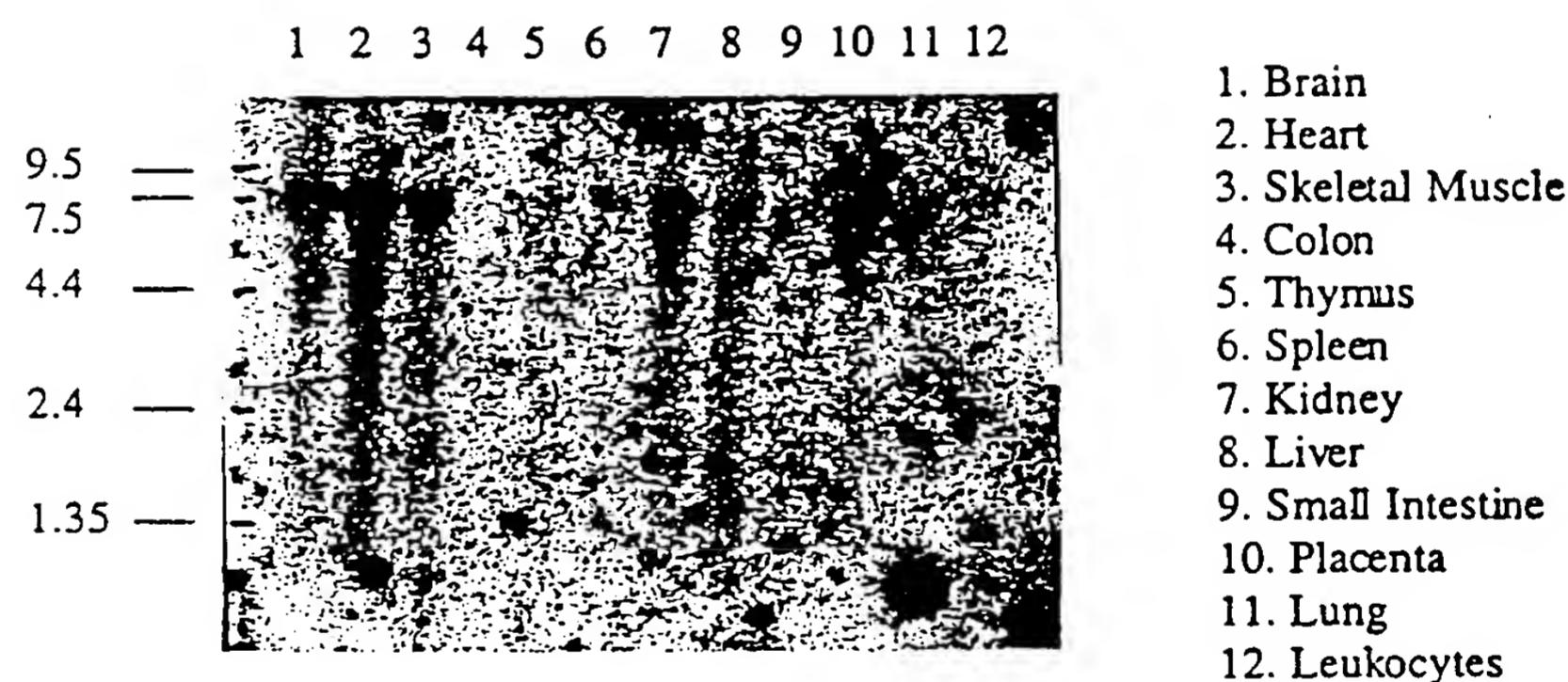
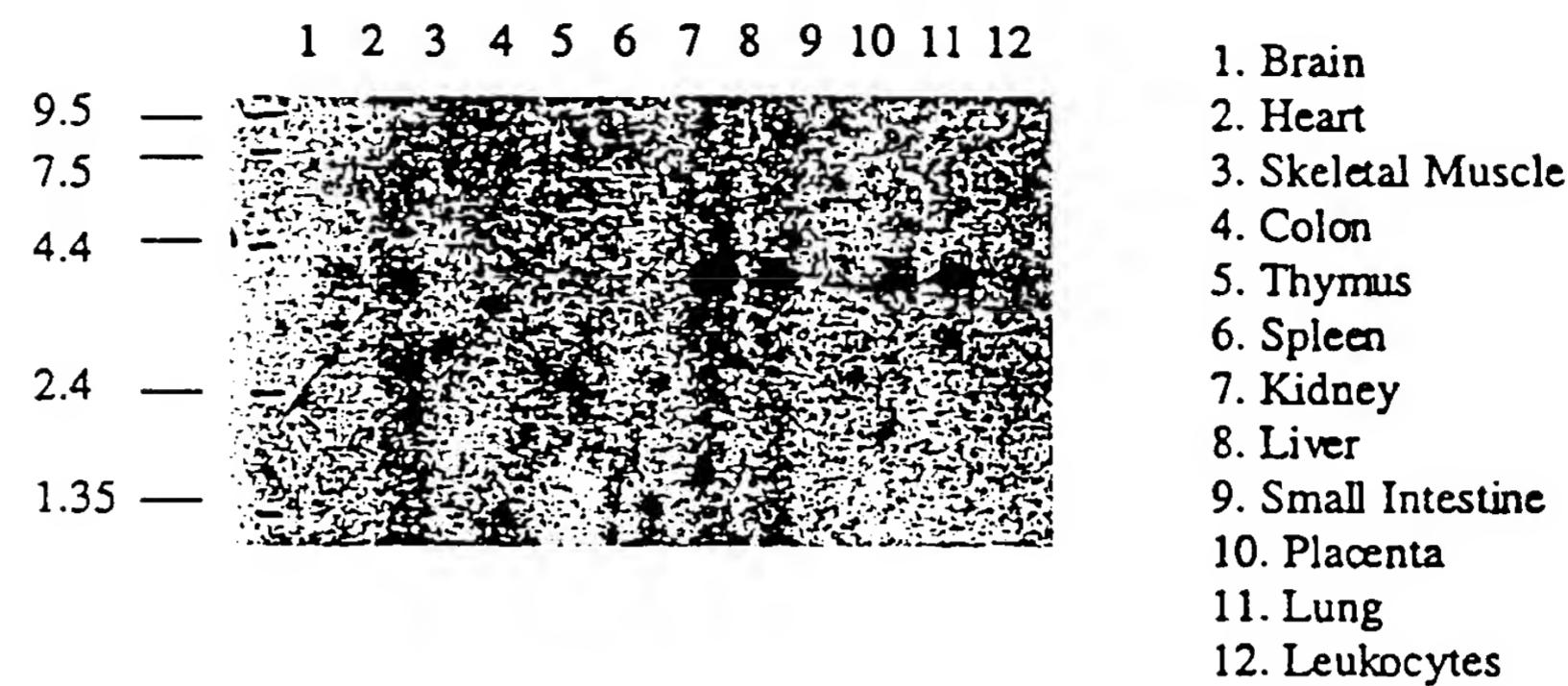


FIG. 6 L

### Gene 605



### Gene 606

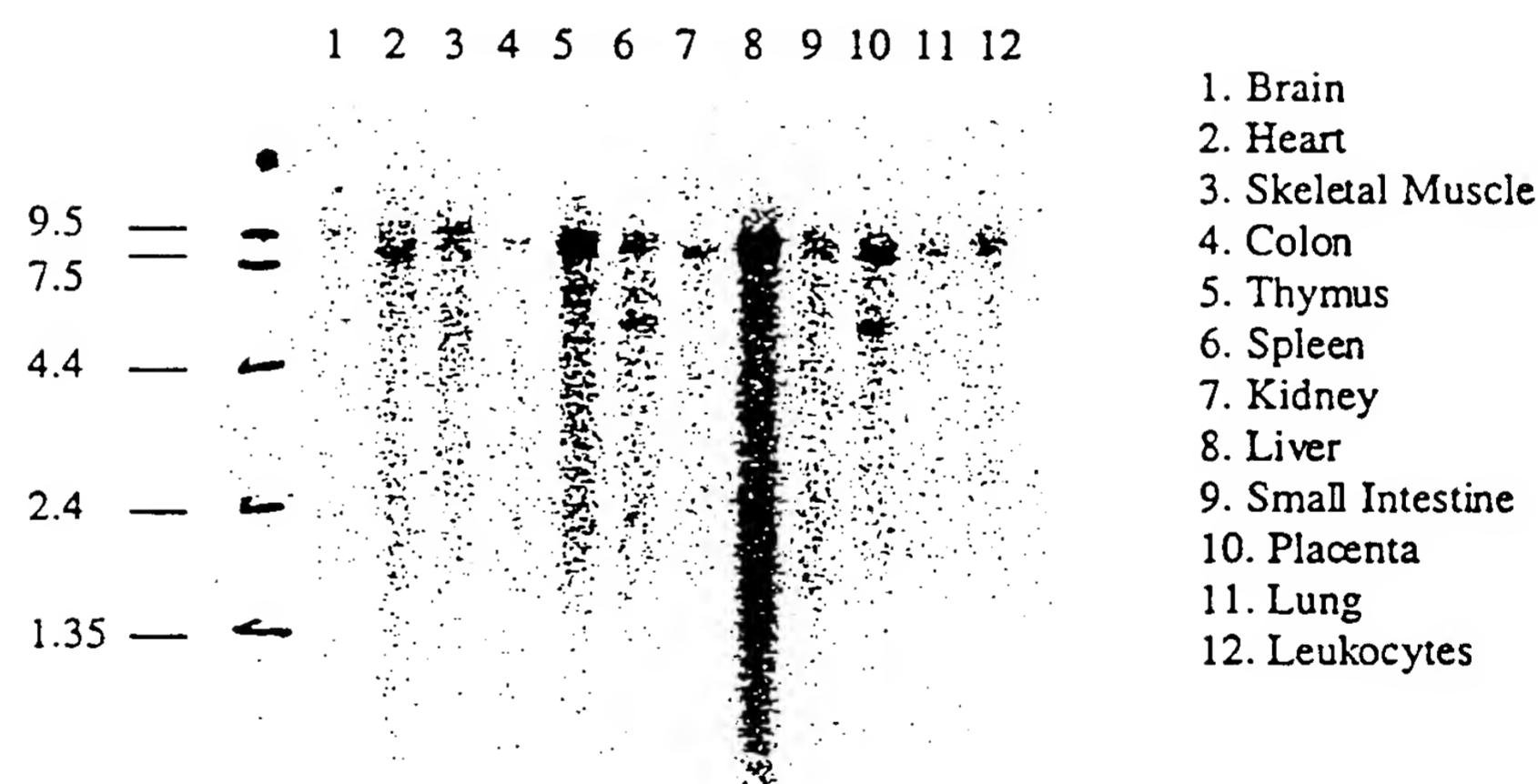
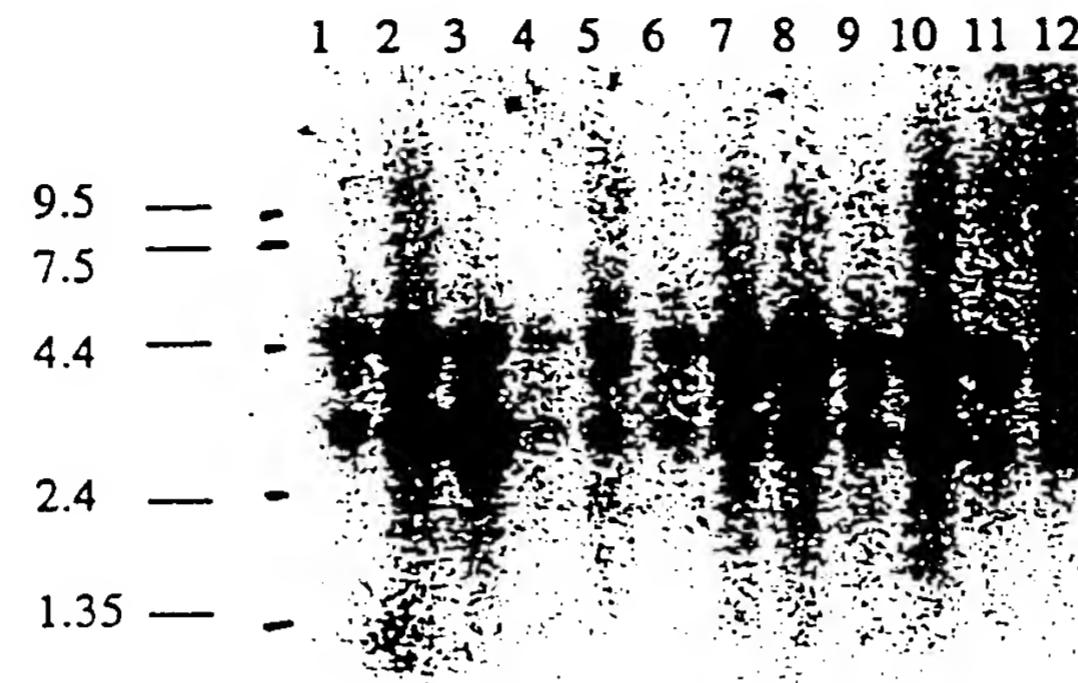


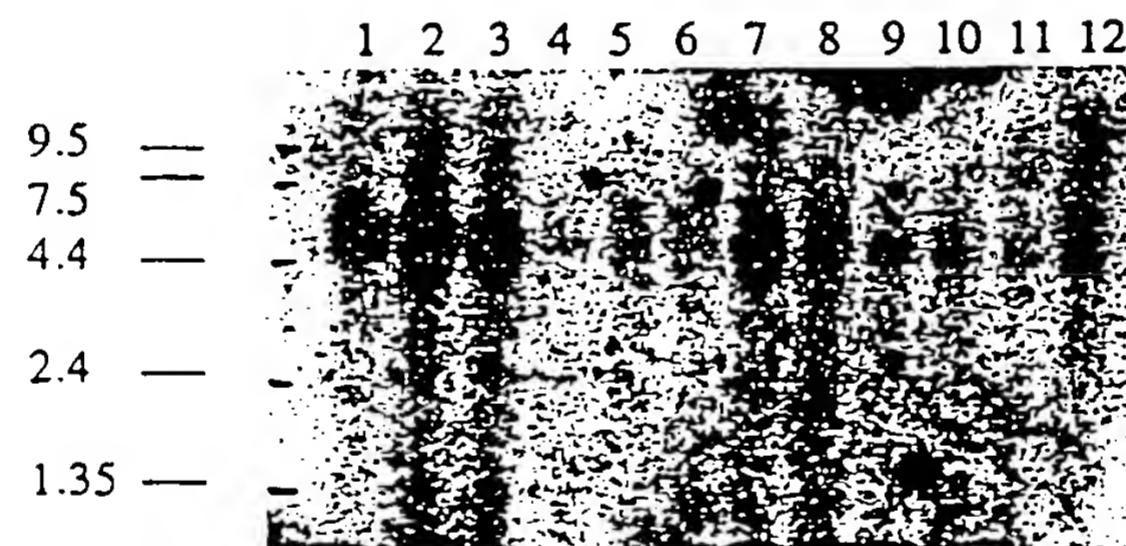
FIG. 6 M

### Gene 608



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

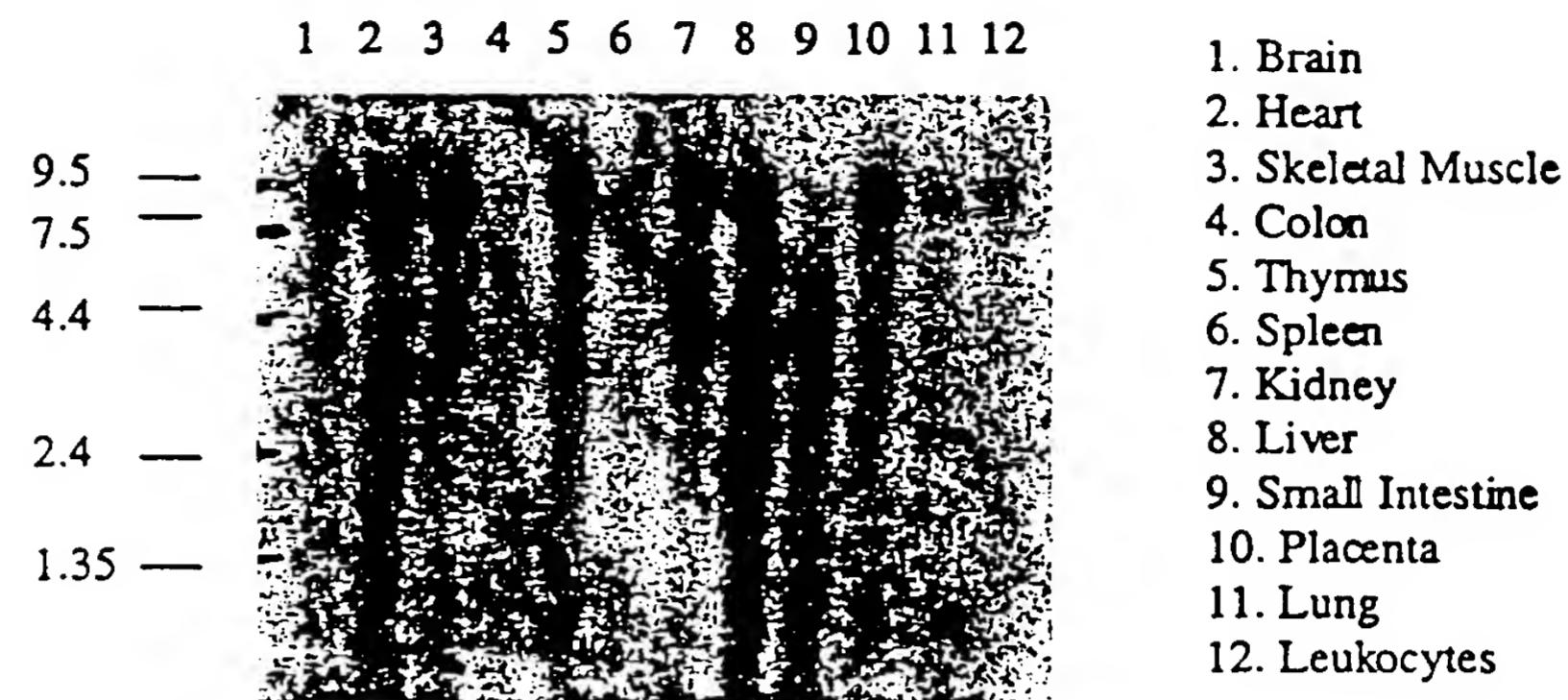
### Gene 611



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 N

### Gene 615



### Gene 617

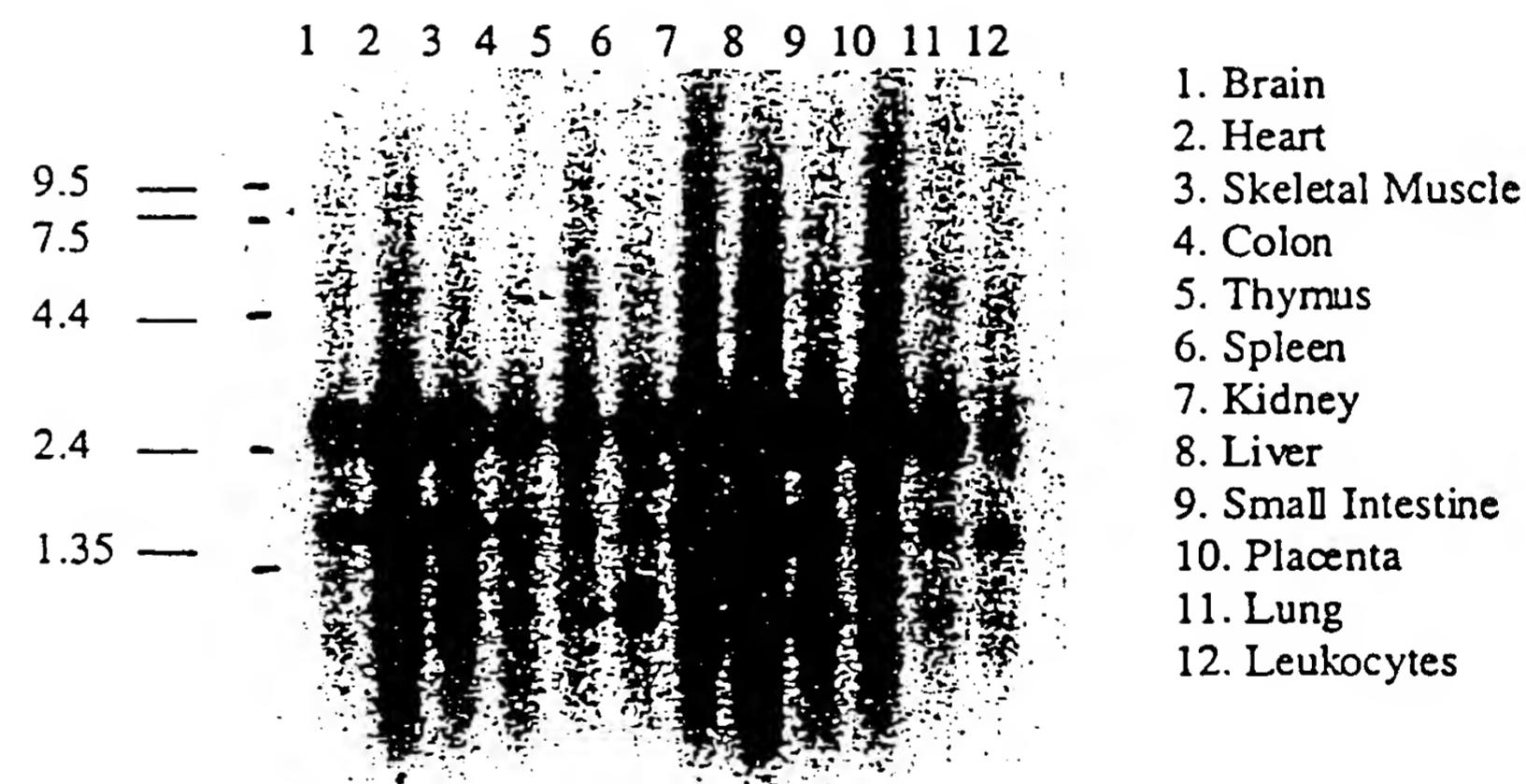
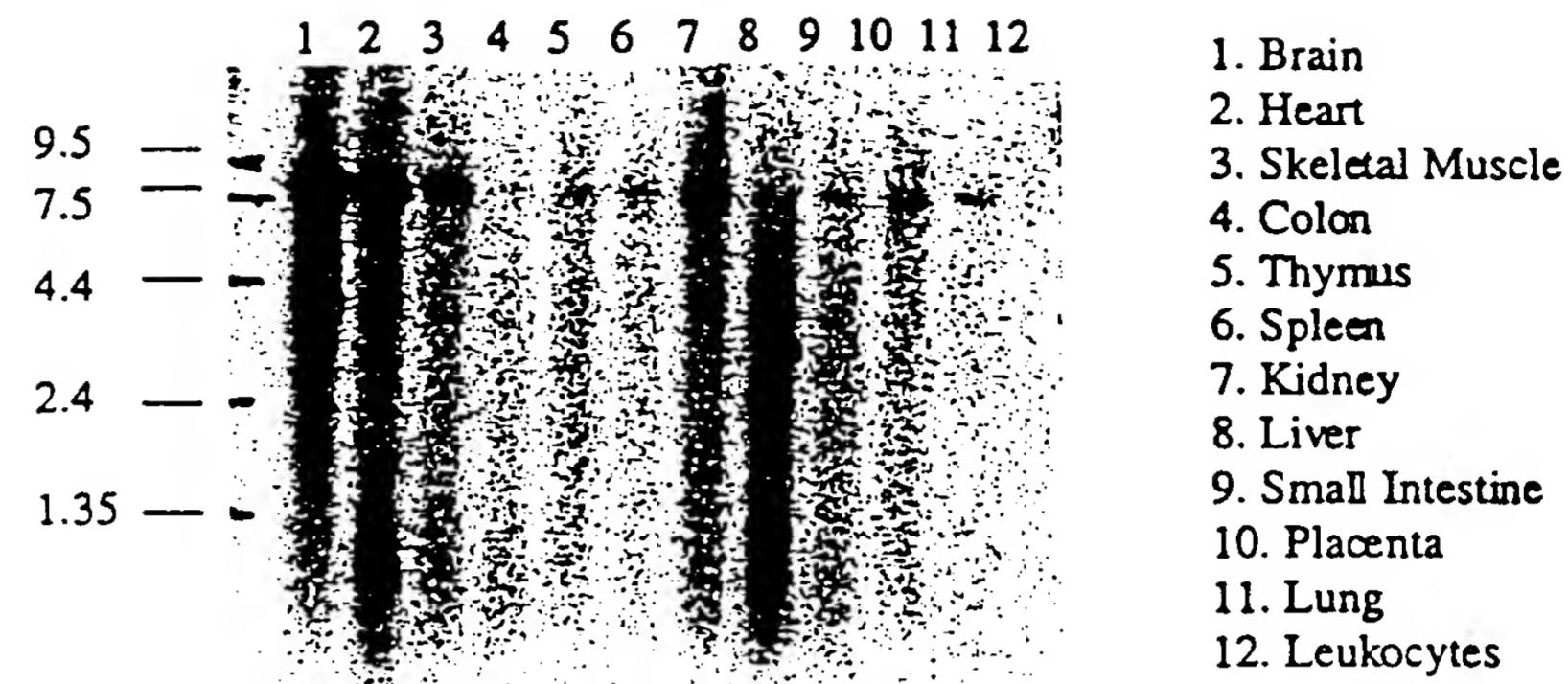


FIG. 6 O

Gene 618



Gene 619

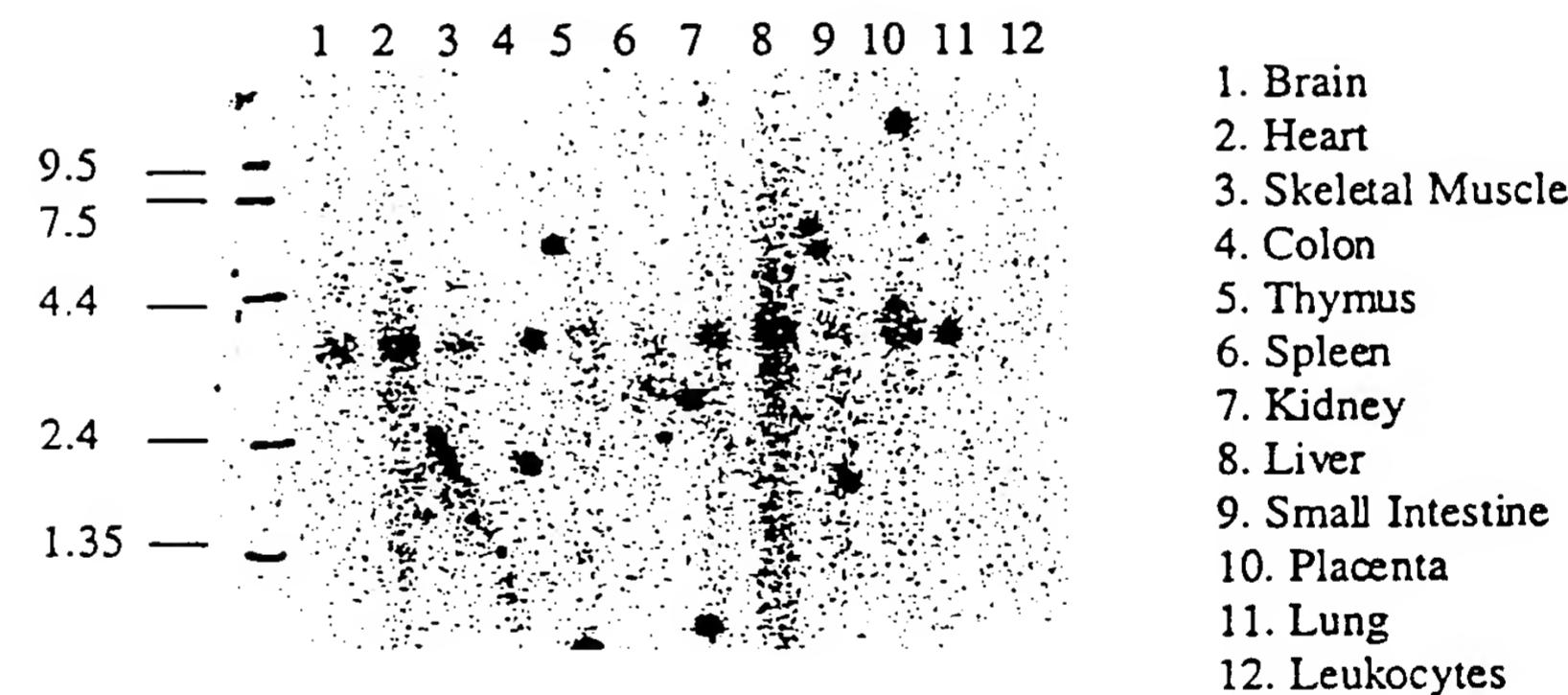
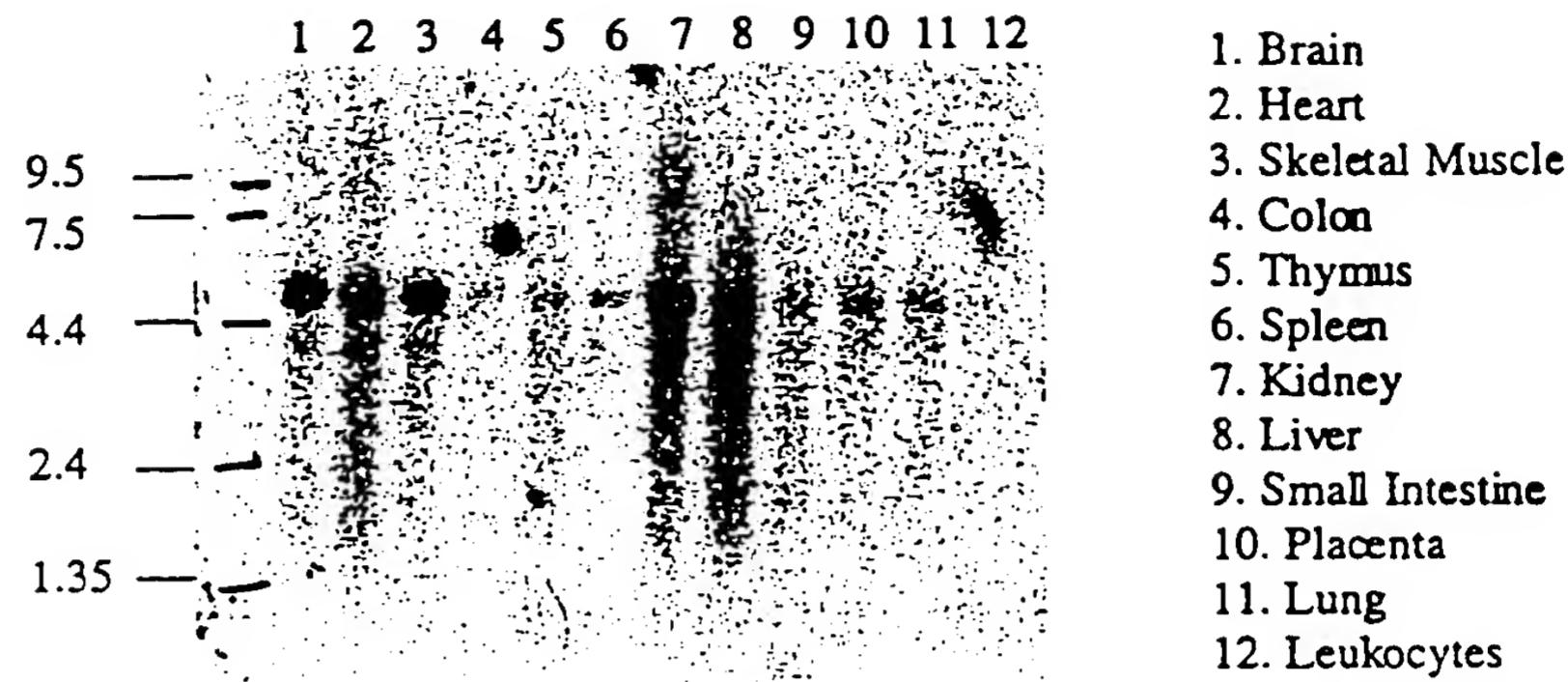


FIG. 6 P

### Gene 621



### Gene 693

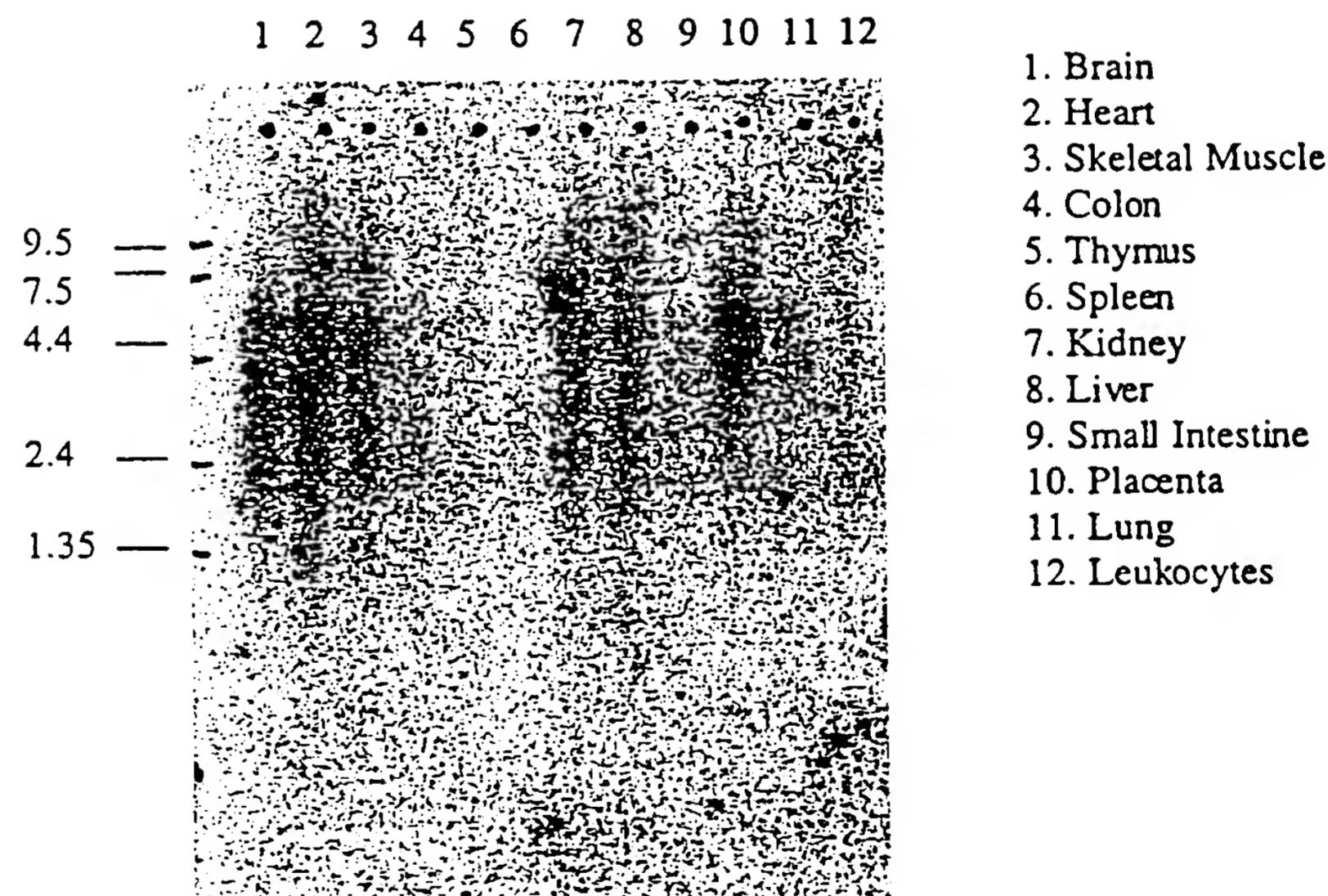
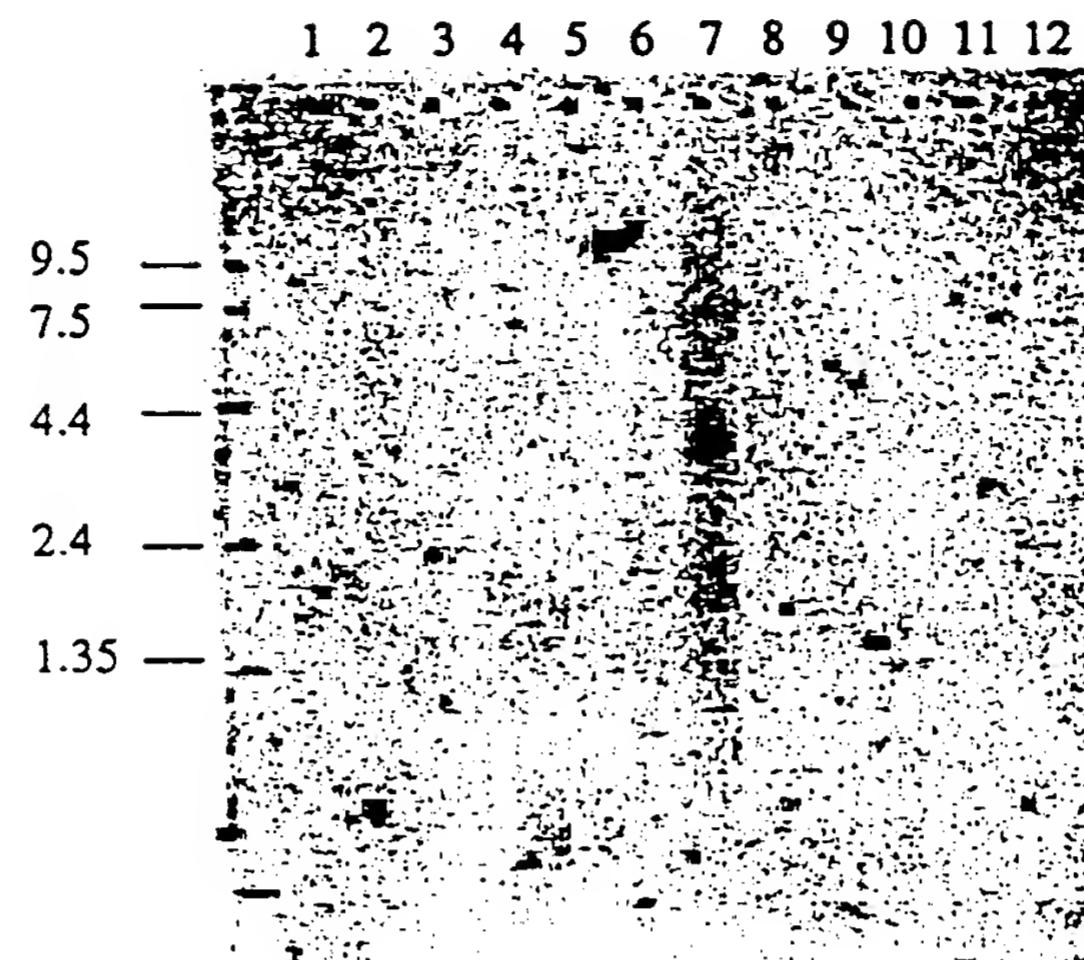


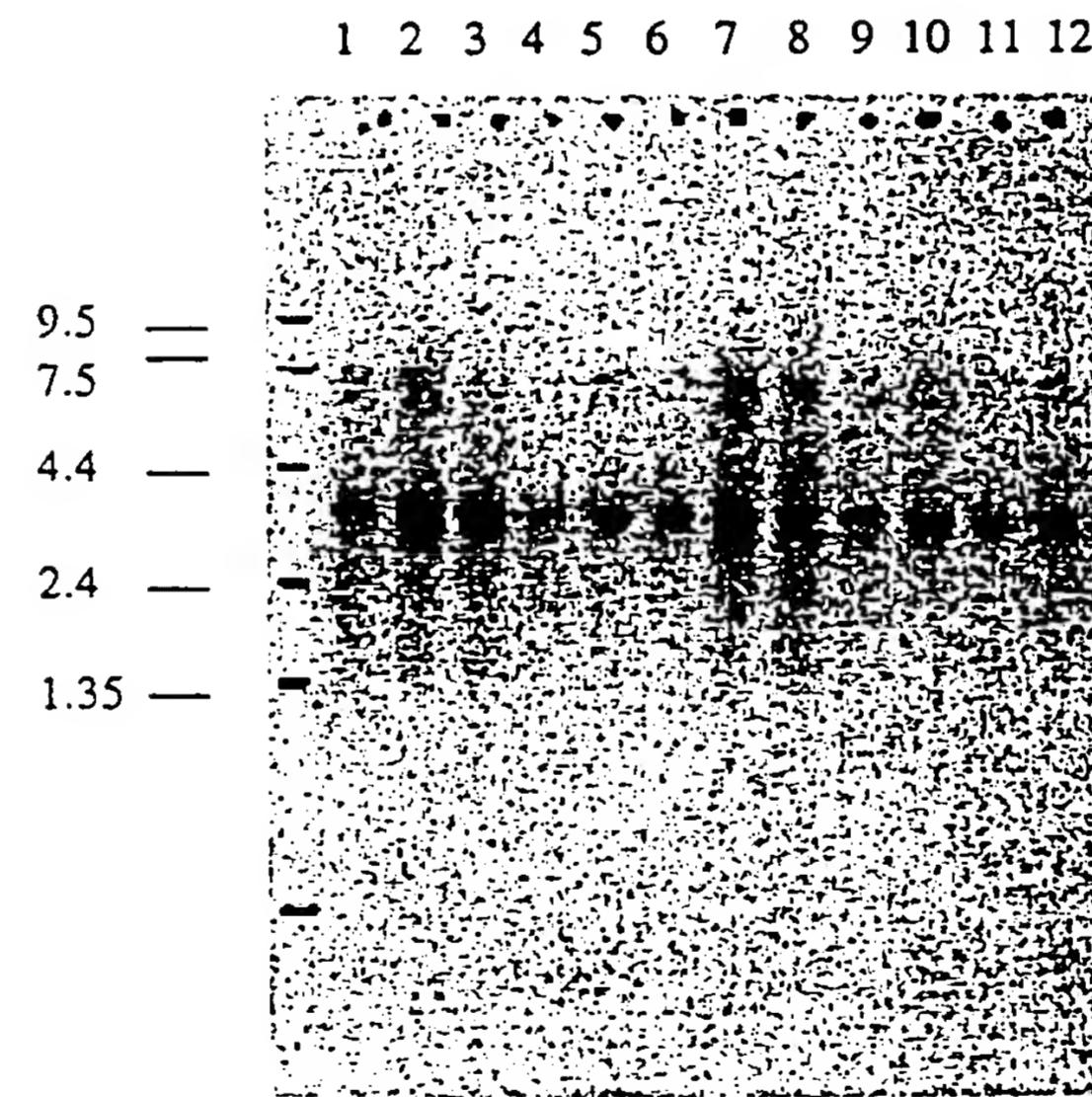
FIG. 6 Q

Gene 698



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

Gene 699



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 R

### Gene 702



### Gene 722

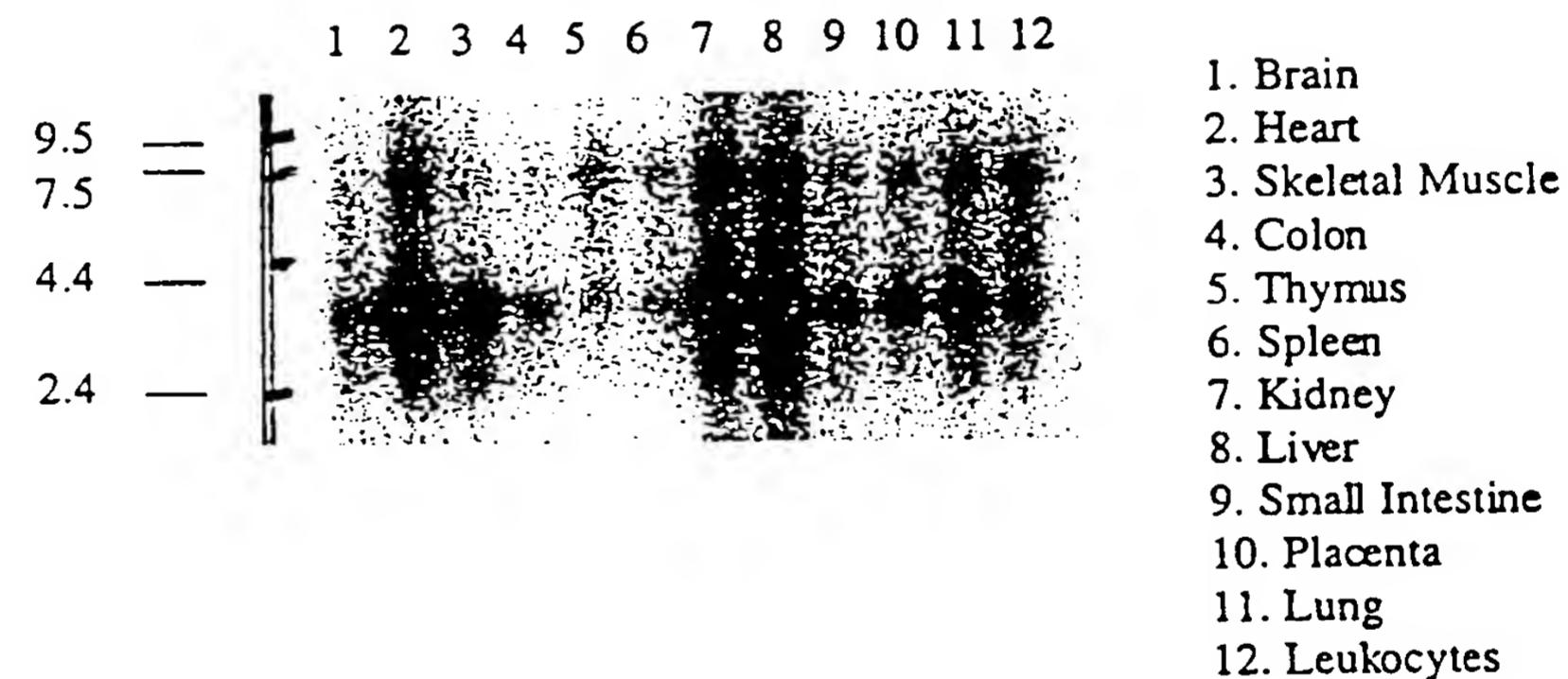
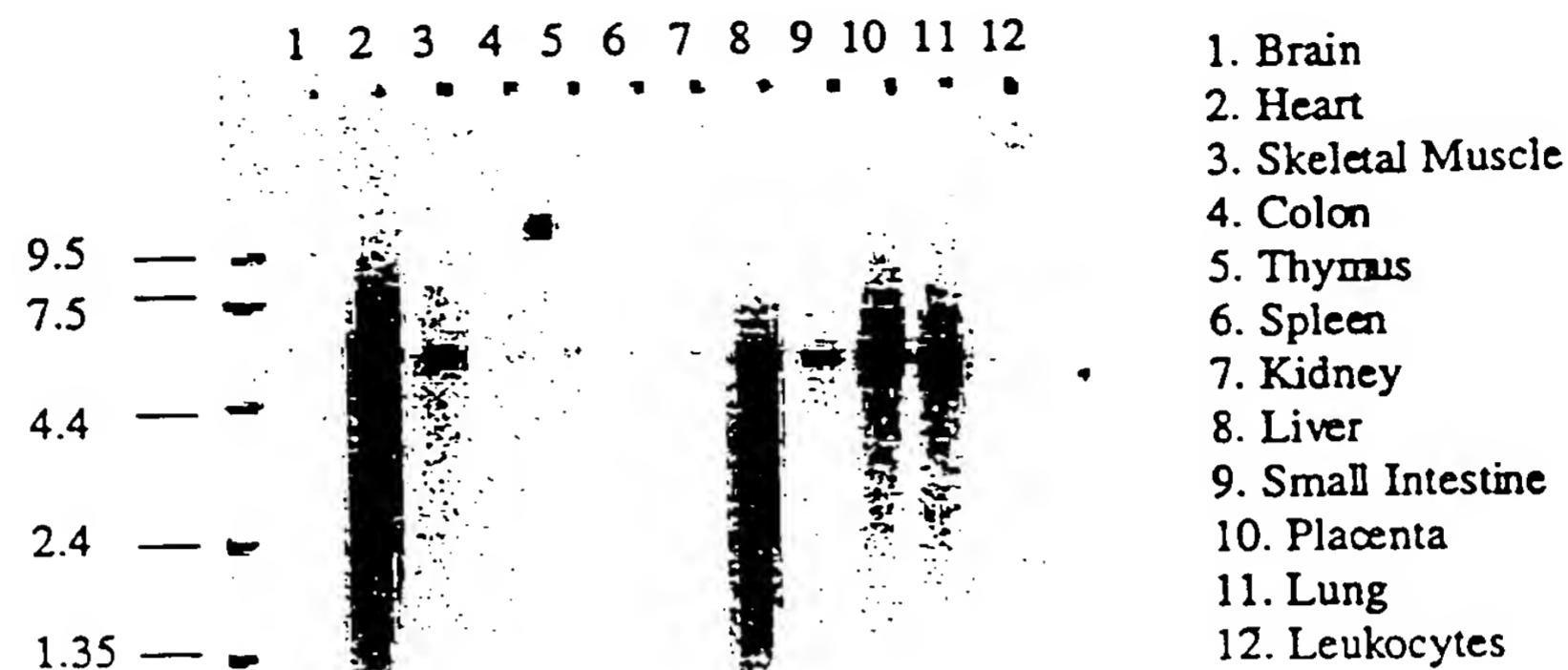


FIG. 6 S

### Gene 751



### Gene 756

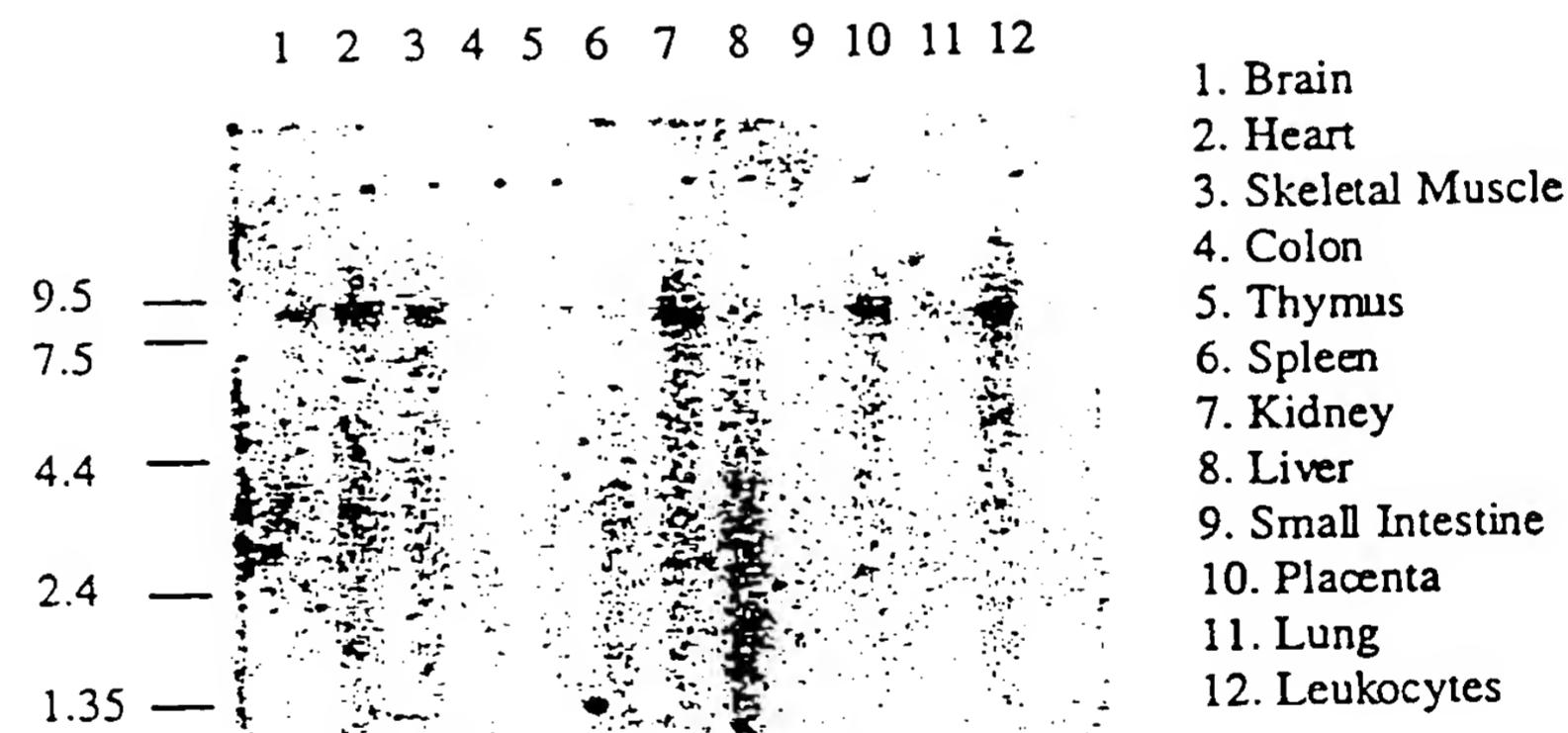
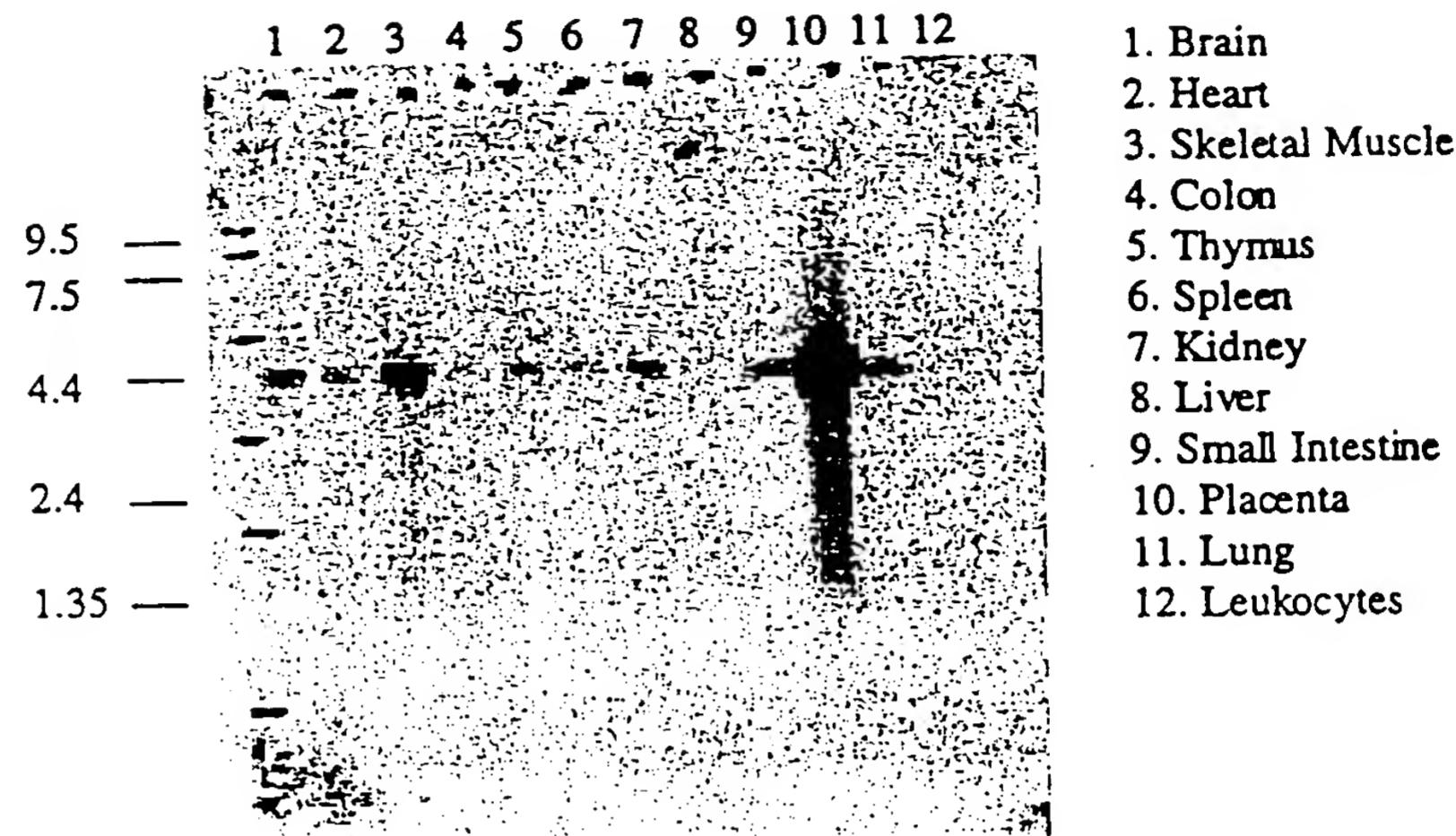


FIG. 6 T

### Gene 757



### Gene 848

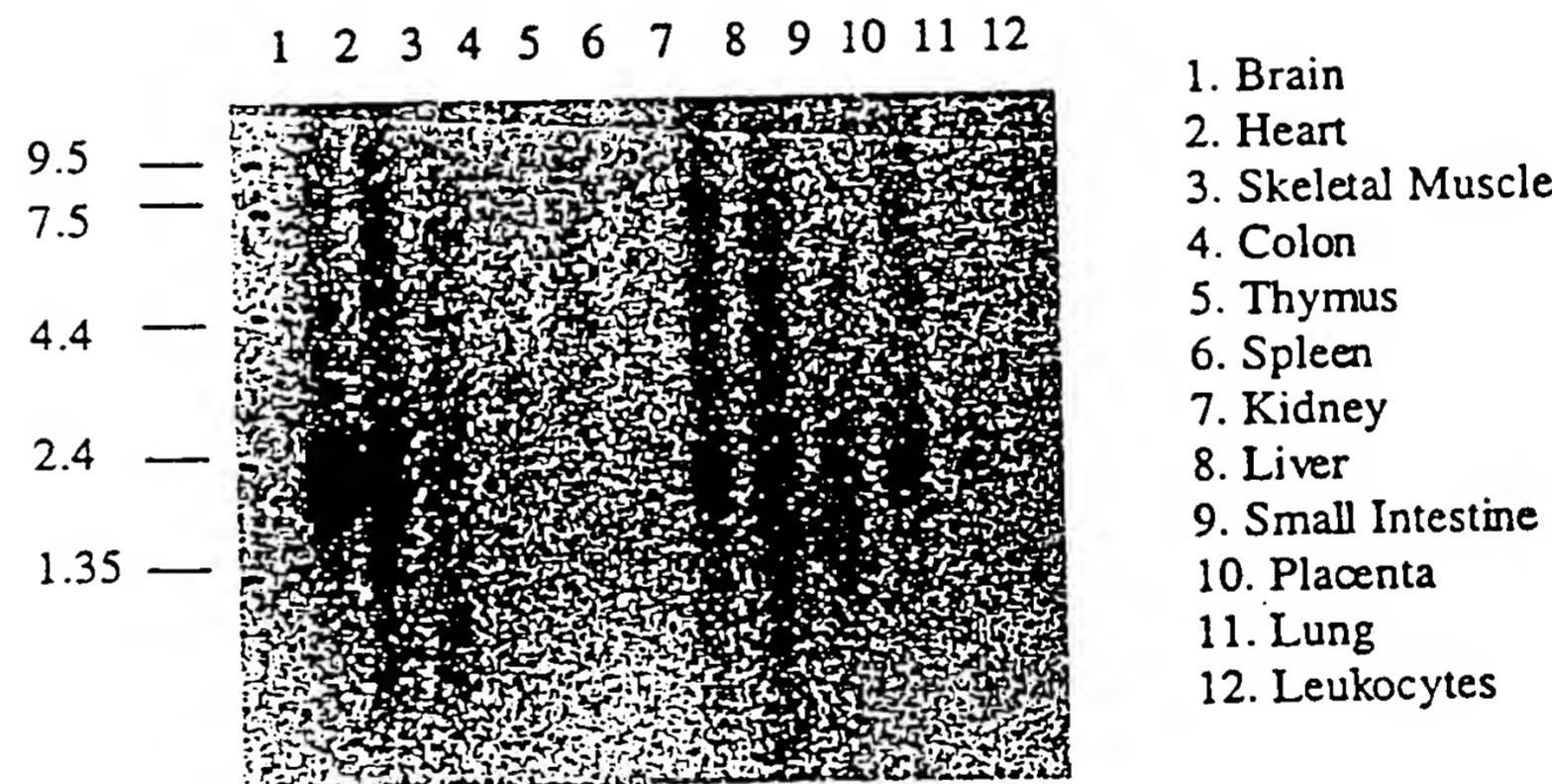


FIG. 6 U

10	30	50
GCTTGCTGTGCCCTGTCAGGAAGAGTAGAGCTCTGGTCCAGCTCCGCGCAGGGAGGGAG		
70	90	110
GCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGATGTTCCAGTATGAGACGAACAAA MetProAlaCysCysSerCysSerAspValPheGlnTyrGluThrAsnLys		
130	150	170
GTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTTCCACGTGATCATC ValThrArgIleGlnSerMetAsnTyrGlyThrIleLysTrpPhePheHisValIleIle		
190	210	230
TTTCCTACGTTGCTTGCTCTGGTGAGTGACAAGCTGTACCAGCGAAAGAGCCTGTC PheSerTyrValCysPheAlaLeuValSerAspLysLeuTyrGlnArgLysGluProVal		
250	270	290
ATCAGTTCTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAAGAGGGAGATCG <u>T</u> GGAG IleSerSerValHisThrLysValLysGlyIleAlaGluValLysGluGluIle <u>Val</u> Glu		
310	330	350
AATGGAGTGAAGAAGTTGGTGCACAGTGCTTGACACCGCAGACTACACCTCCCTTG AsnGlyValLysLysLeuValHisSerValPheAspThrAlaAspTyrThrPheProLeu		
370	390	410
CAGGGAACTCTTCTCGTGTGACAAACTTCTCAAAACAGAAGGCCAGAGCAGCGG GlnGlyAsnSerPhePheValMetThrAsnPheLeuLysThrGluGlyGlnGluGlnArg		
430	450	470
TTGTGTCCCAGTATCCCACCCGCAGGACGCTCTGTTCCCTCTGACCGAGGTTGTAAAAAG LeuCysProGluTyrProThrArgArgThrLeuCysSerSerAspArgGlyCysLysLys		
490	510	530
GGATGGATGGACCCGCAGAGCAAAGGAATTCAAGACCGGAAGGTGTAGTGC <u>A</u> TGAAGGG GlyTrpMetAspProGlnSerLysGlyIleGlnThr <u>Gly</u> ArgCysValVal <u>His</u> GluGly		
550	570	590

FIG. 7 A

AACCAGAAGACCTGTGAAGTCTCTGCCTGGT~~GCCC~~CATCGAGGCAGTGGAAAGAGGCC  
AsnGlnLysThrCysGluValSerAlaTrpCysProIleGluAlaValGluGluAlaPro

610

630

650

CGGCCTGCTCTTGAACAGTGCCGAAAACTCACTGTGCTCATCAAGAACAAATATCGAC  
ArgProAlaLeuLeuAsnSerAlaGluAsnPheThrValLeuIleLysAsnAsnIleAsp

670

690

710

TTCCCCGGCCACAACTACACCACGAGAAACATCCTGCCAGGTTAACATCACTTGTACC  
PheProGlyHisAsnTyrThrArgAsnIleLeuProGlyLeuAsnIleThrCysThr

730

750

770

TTCCACAAGACTCAGAATCCACAGTGTCCCATTTCGACTAGGAGACATCTCCGAGAA  
PheHisLysThrGlnAsnProGlnCysProIlePheArgLeuGlyAspIlePheArgGlu

790

810

830

ACAGGCGATAATTTTCAGATGTGGCAATTCAGGGCGGAATAATGGGCATTGAGATCTAC  
ThrGlyAspAsnPheSerAspValAlaIleGlnGlyGlyIleMetGlyIleGluIleTyr

850

870

890

TGGGACTGCAACCTAGACCGGTTGGTCCATCACTGCCGTCCAAATACAGTTCCGT  
TrpAspCysAsnLeuAspArgTrpPheHisHisCysArgProLysTyrSerPheArgArg

910

930

950

CTTGACGACAAGACCACCAACGTGTCTTGCTACAACTTCAGATACGCCAAG  
LeuAspAspLysThrThrAsnValSerLeuTyrProGlyTyrAsnPheArgTyrAlaLys

970

990

1010

TACTACAAGGAAAACAATGTTGAGAAACGGACTCTGATAAAAGTCTCGGGATCCGTTT  
TyrTyrLysGluAsnAsnValGluLysArgThrLeuIleLysValPheGlyIleArgPhe

1030

1050

1070

GACATCCTGGTTTGGCACCCGGAGGAAAATTGACATTATCCAGCTGGTTGTACATC  
AspIleLeuValPheGlyThrGlyGlyLysPheAspIleIleGlnLeuValValTyrIle

1090

1110

1130

GGCTAACCCCTCTCCTACTTCGGTCTGGCCACTGTGTTCATCGACTTCCTCATCGACACT  
GlySerThrLeuSerTyrPheGlyLeuAlaThrValPheIleAspPheLeuIleAspThr

FIG. 7 B

1150

1170

1190

TACTCCAGTAAC TGCTGCGCTCCCATATTATCCCTGGTGC  
AAGTGCTGTCAGCCCTGT  
TyrSerSerAsnCysCysArgSerHisIleTyrProTrpCysLysCysCysGlnProCys

1210

1230

1250

GTGGTCAACGAATACTACTACAGGAAGAAGTGC  
GAGTCCATTGTGGAGCCAAAGCCGACA  
ValValAsnGluTyrTyrArgLysLysCysGluSerIleValGluProLysProThr

1270

1290

1310

TTAAAGTATGTGCTTGTGGATGAATCCCACATTAGGATGGTGAACCAGCAGCTACTA  
LeuLysTyrValSerPheValAspGluSerHisIleArgMetValAsnGlnGlnLeuLeu

1330

1350

1370

GGGAGAACGTTGCAAGATGTCAAGGGCCAAGAAGTCCCAAGACCTGCGATGGACTTCACA  
GlyArgSerLeuGlnAspValLysGlyGlnGluValProArgProAlaMetAspPheThr

1390

1410

1430

GATTGTCAGGCTGCCCTGGCCCTCCATGACACACCCCCGATTCTGGACAACCAGAG  
AspLeuSerArgLeuProLeuAlaLeuHisAspThrProProIleProGlyGlnProGlu

1450

1470

1490

GAGATACAGCTGCTTAGAAAGGAGGCGACTCCTAGATCCAGGGATAGCCCCGTCTGGTGC  
GluIleGlnLeuLeuArgLysGluAlaThrProArgSerArgAspSerProValTrpCys

1510

1530

1550

CAGTGTGGAAGATGCCTCCCATCTCAACTCCCTGAGAGGCCACAGGTGCCTGGAGGAGCTG  
GlnCysGlyArgCysLeuProSerGlnLeuProGluSerHisArgCysLeuGluLeu

1570

1590

1610

TGCTGCCGGAAAAGCCGGGGCCTGCATCACCACTCAGAGCTGTTAGGAAGCTGGTC  
CysCysArgLysLysProGlyAlaCysIleThrSerGluLeuPheArgLysLeuVal

1630

1650

1670

CTGTCCAGACACGTCTGCAGTTCCCTCTGCTCTACCAGGAGCCCTTGCTGGCGCTGGAT  
LeuSerArgHisValLeuGlnPheLeuLeuTyrGlnGluProLeuLeuAlaLeuAsp

1690

1710

1730

**FIG. 7 C**

GTGGATTCCACCAACAGCCGGCTGCCGC ACT GTGCC TACAGGTGCTACGCCACCTGGCGC  
ValAspSerThrAsnSerArgLeuArgHisCysAlaTyrArgCysTyrAlaThrTrpArg

1750

1770

1790

TTCGGCTCCCAGGACATGGCTGACTTGCCATCCTGCCAGCTGCCGCTGGAGGATC  
PheGlySerGlnAspMetAlaAspPheAlaIleLeuProSerCysCysArgTrpArgIle

1810

1830

1850

CGGAAAGAGTTCCAAAGAGTGAAGGGCAGTACAGTGGCTTCAAGAGTCCTTACTGAAGC  
ArgLysGluPheProLysSerGluGlyGlnTyrSerGlyPheLysSerProTyrEnd

1870

1890

1910

CAGGCACC GTGGCTCACGTCTGTAATCCCAGCGCTTGGAGGCCGAGGCAGGATCA

1930

1950

1970

CCTGAGATCGGGAGTTGGAGACCCGCCTGGCTAACAAAGGCAGAACCTGTCTGTACTAAA

1990

2010

2030

AATA CAAAAAATCAGCCAGACATGGTGGCATGCACCTGCAATCCCAGCTACTCGGGAGGCT

2050

2070

2090

GAGGCACAAGAATCACTGAACCCGGGAGGCAGAGGTTGTAGTGAGCCCAGATTGTGCCA

2110

2130

2150

CTGCTCTCCAGCCTGGGAGGCACAGCAAACTGTCCCCAAAAAAAAAGAGTCCTTAC

2170

2190

2210

CAATAGCAGGGCTGCAGTAGCCATGTTAACATGACATTACAGCAACTTGAACTTCAC

2230

2250

2270

CTGCAAAGCTCTGTGGCCACATTTCAGCCAAAGGGAAATATGCTTCATCTTCTGTTGC

2290

2310

2330

TCTCTGTGTCTGAGAGCAAAGTGACCTGGTAAACAAACCAGAAATCCCTCTACATGGACT

2350

2370

2390

FIG. 7 D

CAGAGAAAAGAGATTGAGATGTAAGTCTCAACTCTGTCCCCAGGAAGTTGTGACCC  
2410 2430 2450  
GGCCTCTCACCTCTGTGCCTCTGTCTCCTTGTTGCCAACTACTATCTCAGAGATATTGT  
2470 2490 2510  
GAGGACAAATTGAGACAGTGCACATGAACGTCTTTAATGTGTAAAGATCTACATGAAT  
2530 2550 2570  
GCAAAACATTCATTATGAGGTAGACTAGGATAATGTCCAACAAAAACAAACCCTTT  
2590 2610 2630  
CATCCTGGCTGGAGAACATGGAGAACTAAAGGTGGCCACAAATTCTTGACACTCAAGTC  
2650 2670 2690  
CCCCAAGACCTAAGGGTTTATCTCCTCCCTTGAATATGGGTGGCTCTGATTGCTTAT  
2710 2730 2750  
CCAAAAGTGGAAAGTGACATTGTGTCAGTTCACTGATCTTAAGAGGCTGACAGCTT  
2770 2790 2810  
CTACTTGCTGTCCCTTGGAACTCTTGCTATCGGGAGGCCAGGCCATTAAAAGTCTG  
2830 2850 2870  
CCTATCCTGGCCAGGTGTGGCTCACACCTGTAATCCCAGCACTTGGGAGACCAAGG  
2890 2910 2930  
CGGGCGGATCACTAAAGTCAGGAGTCCAAGACCAGACTGCCAACATGGTGAACCGTA  
2950 2970 2990  
TCTCTAATAAAAATACAAAAATTAGCTGGCATGGTGGCAGCTGTAGTCAGCTAT  
3010 3030 3050  
CAAGAGGCTGAGACAGGAGAAACACTTGAACCTGGAGGTGGAGGTTGCATTGAGCTGAG

FIG. 7 E

3070                    3090                    3110  
ATCGTGCCACTGCACTCCAGGCTGGGTGACAGAGCGAGACTCCATCTCAAAAAAAAAAA  
  
3130                    3150                    3170  
AAAAGAAAAAAATGTCTGCCTATCCTGAGACTGCCCTGCTGTGAGGAAGCCCAAGCA  
  
3190                    3210                    3230  
GTCACGTGGACAGTGCTGACCAGCCCCAGCTTCAAGCCATCCAAGCCCAGTCACCAAA  
  
3250                    3270                    3290  
CATGAGAGAGAAGAACCTTCAGGTGATTCTGGACTCCACTAACATATGACTGATAACCGC  
  
3310                    3330                    3350  
ATGATACATCCCAAGTGAGAACTGCCCTAAATCCAGAAAACCACATTGCTATCTTAAG  
  
3370                    3390                    3410  
TCCCTAACGTTGGGCTTATTGTTCCACAGAACAGGTAACGGAACAGAGGGCAAGCC  
  
3430                    3450                    3470  
TGATGAATGGCACACAGACTCAGCCCATACTTCCCTGGTTCTAATGTTCTCAGGGAGC  
  
3490                    3510                    3530  
CCGGACCAACCCTGGAGCCTCAGGAACCTAGGTTCCACTGGACAGTTCTAGAAGGGCT  
  
3550                    3570                    3590  
ATAGACCAAATCAGGTAACTCACCAAGACCAGCCTGGAATCTATCAAATCTAACTGCTGA  
  
3610                    3630                    3650  
GCTACCCAGTGCATTCCGATCCTCATCACATTCTTGAACGGGCCGGCGTGGTGGC  
  
3670                    3690                    3710  
TCACGCCCTGTAATCCCAGCCTTGGGAGGCTGAGGCGGGTGGATCACCTGAGGTCAAGGA

FIG. 7 F

3730

3750

3770

GTTCGAGACCAGCCTGGCCAACATGGTGAGACCCCTGTCTACTAAGAATACAAAAATT

3790

3810

3830

GGTGGGGTGGCGGTGGCGCCTGTAATCCCAGCTACTGGGAGGCTGAGGCAGGAGAAC

3850

3870

3890

TCTTGAACCTGGAAGGTGGAGGTTGCAATAAGCCGAGATAGTGCCACTGCAC

3910

3930

3950

AGATAACAGAGCAAGACTCTGTCTAAAAACAACAACAACAACAAATTCTAT

3970

3990

4010

GACTGAAAGTGA

4030

4050

4070

ACTAAAAAGCTGGCTTATGCCATTAACACTCTGTACTTTGCAGCCAAT

4090

4110

4130

CAGAACTGACGCAGTCTGGGTGCTAGCTGCTCAAAAGCAACCCACACCACACTTTACC

4150

4170

4190

CTTCAGGATTCTCTTCTGGTTGGTCACTAGAGTTGGCTATTATCTGTTCTAAC

4210

4230

4250

AATAGCTATTTATCGAATAGTTAGAGACCACTATTAAATATTGTGACTGATGAAGGAT

4270

4290

4310

CTGTGAATTTTATATGTTCTAAGAGTTACCATTGATACCTTTAAAAACCAGC

4330

4350

4370

AGCTTTCTACTATATTGAAAACAGCATGAATAAAACCATTGATACAGGGTTT

4390

4410

4430

**FIG. 7 G**

TATTTGGCTTAAACTCAGGAACCAAGTTAATTATGCCAGATTGAACTTGATTTACT

4450

4470

4490

ACCTTTCAAAGATATTTAAAAAGTGGATTACTACATATGATTCTTGGAGCTTACAT

4510

4530

4550

TTCTTACTTCACGAATTCTATGTCACTGTTACAAGTTCCATTCTGATGGCTCTGGGC

4570

4590

4610

CTTTGTACCTTGTGTTGGTGCCTTATTCTAGTATGTTCTATCACCTTAATGAGGCC

4630

4650

4670

GCAGATGGAGTCAGAATGTGAAATTACAAATAATCACTGGATCCATCTACTGTTCCAT

4690

4710

4730

CACCTCCCCACTGATGCTCTGGCGAGAGAGTGATGTGTCACTCAACTGTGTGTAATA

4750

4770

4790

TGTCAGACACGTCCTACAATAAACAGGCGTCATATTGTATTATTTAGTTACTGTAGA

4810

4830

4850

AAATAATGTACCGCCAAAGGTGATGAGAGTCACGTTGTAGGATCTGTTCTTATAC

4870

4890

4910

TTAAAGACAGACTTCTGCTACGGTAATTGCCAGTATTGATGGCTCCTTGTGTCAGA

4930

4950

4970

AGAGAAGGGATCTGCTTCTTGGCTGATTCACATAGCATTGTAATAGACATGCATT

4990

5010

5030

TCTCTTCTAAAGGGAGTAACCTTAAACCCTCCTGATTTAGCCTGGCAATGTAAG

5050

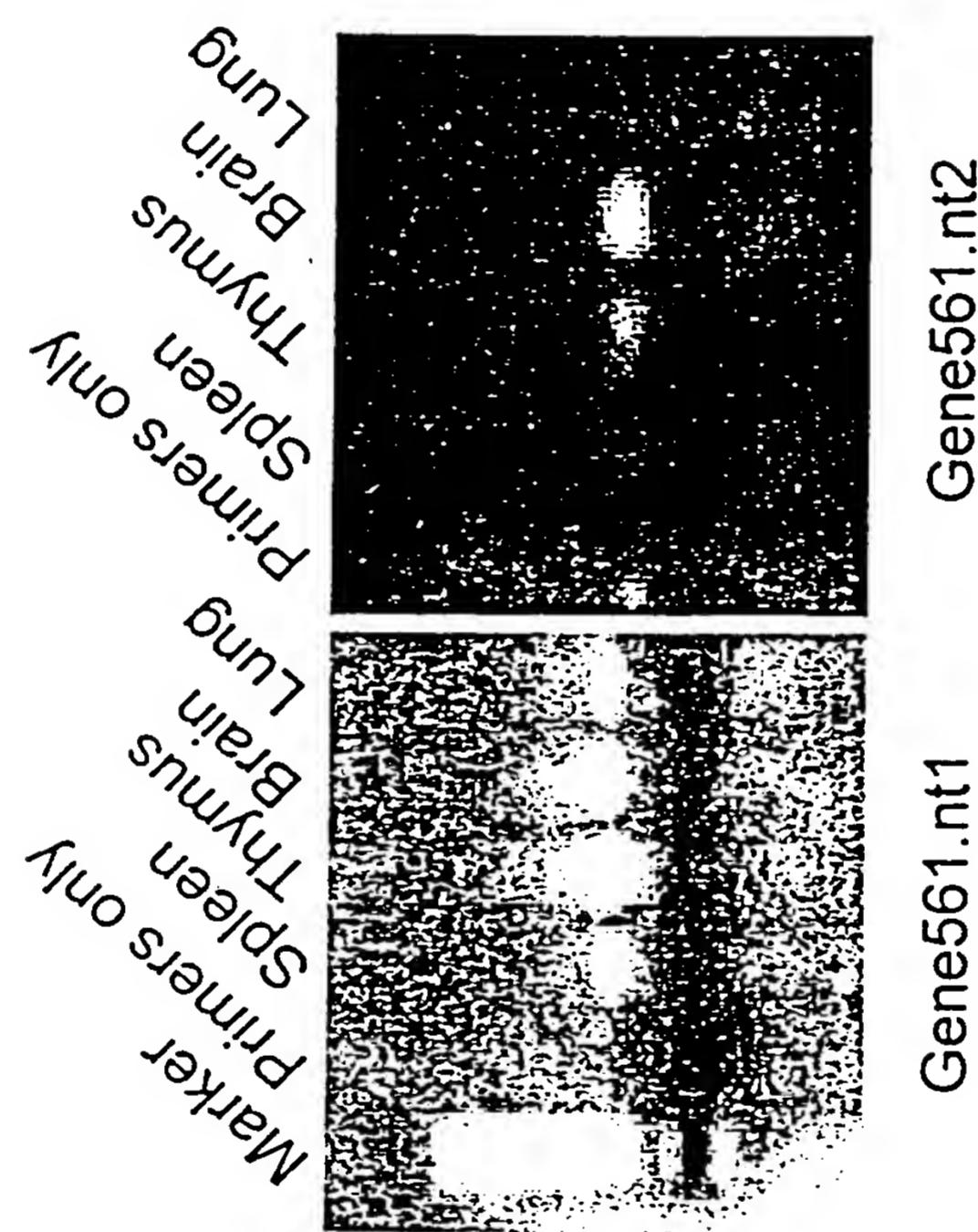
5070

TGTCCTTAATGTGACTGTTGATAATTAAAAAGGTATATAATT

FIG. 7 H

8  
FIG.

## RT/PCR of Gene561.nt1 and Gene561.nt2



10                   30                   50  
TCGAAACAGCTGCCGGCTGGTCCC GGCGAGGCCGGCGCAGGGAGGGAGGAGCCGCCGG  
  
70                   90                   110  
GCTGTGGGGCGCCGCGAGCTGGGCCGGCTCGGTGTGCCCGCGCCGCCAGCCCCGCTCCA  
  
130                 150                 170  
GACGCGCCACCTGGCGCTCCAAGAACAGAGGCCGAAGTTGCCGGCCGTGAGTTGGAGC  
  
190                 210                 230  
TCGCGCCGGGCCGCTGCGCCGGAGCTCCGGGGCTTCCCTCGCTTCCC GGATTGTTG  
  
250                 270                 290  
CAAACTTGCTGCTCTCCGCGCGGCCCAACTCGGCGGACGCCGGCGGGAGAGCCG  
  
310                 330                 350  
AGCCGGGGCGCTGTGCGCAGCGCTCGGCCAGGCCGGGGCATGGCGGGGGCGA  
  
370                 390                 410  
GCAGGGGTGGAGAGCCGGGCCAGCAGCACGCCGTGCCGGAGCGGGCGCTGAGGGG  
  
430                 450                 470  
CGCGGAGCTCCCCCGAGGACACGTCCAACGCCAGCATGCAGGCCGGCCCCGCCTG  
MetGlnArgProGlyProArgLeu  
  
490                 510                 530  
TGGCTGGT CCTGCAGGTGATGGCTCGTGCGCCGCCATCAGCTCCATGGACATGGAGCGC  
TrpLeuValLeuGinValMetGlySerCysAlaAlaIleSerSerMetAspMetGluArg  
  
550                 570                 590  
CCGGGCGACGGCAAATGCCAGCCATCGAGATCCCGATGTGCAAGGACATCGGCTACAAC  
ProGlyAspGlyLysCysGlnProIleGluIleProMetCysLysAspIleGlyTyrAsn  
  
610                 630                 650

FIG. 9 A

ATGACTCGTATGCCAACCTGATGGGCCACGAGAACCGCGAGGCAGCCATCCAGTTG  
MetThrArgMetProAsnLeuMetGlyHisGluAsnGlnArgGluAlaAlaIleGlnLeu

670

690

710

CACGAGTTCGCGCCGCTGGTGGAGTACGGCTGCCACGGCACCTCCGCTTCTCCTGTGC  
HisGluPheAlaProLeuValGluTyrGlyCysHisGlyHisLeuArgPhePheLeuCys

730

750

770

TCGCTGTACGCGCCGATGTGCACCGAGCAGGTCTCTACCCCCATCCCCGCCTGCCGGGTC  
SerLeuTyrAlaProMetCysThrGluGlnValSerThrProIleProAlaCysArgVal

790

810

830

ATGTGCGAGCAGGCCGGCTCAAGTGTCTCCCGATTATGGAGCAGTTCAACTCAAGTGG  
MetCysGluGlnAlaArgLeuLysCysSerProIleMetGluGlnPheAsnPheLysTrp

850

870

890

CCCGACTCCCTGGACTGCCGGAAACTCCCCAACAAAGAACGACCCAACTACCTGTGCATG  
ProAspSerLeuAspCysArgLysLeuProAsnLysAsnAspProAsnTyrLeuCysMet

910

930

950

GAGGCGCCAACAACGGCTCGGACGAGCCCACCCGGGGCTGGGCCTGTTCCGCCGCTG  
GluAlaProAsnAsnGlySerAspGluProThrArgGlySerGlyLeuPheProProLeu

970

990

1010

TTCCGGCCGCAGCGGCCAACAGCGCGCAGGAGCACCCGCTGAAGGACGGGGCCCCGGG  
PheArgProGlnArgProHisSerAlaGlnGluHisProLeuLysAspGlyGlyProGly

1030

1050

1070

CGCGGGCTGCGACAACCCGGCAAGTTCCACCACGTGGAGAAGAGCGCGTGTGCGCG  
ArgGlyGlyCysAspAsnProGlyLysPheHisHisValGluLysSerAlaSerCysAla

1090

1110

1130

CCGCTCTGCACGCCGGCTGGACGTGTACTGGAGCCGCGAGGACAAGCGCTTCGCAGTG  
ProLeuCysThrProGlyValAspValTyrTrpSerArgGluAspLysArgPheAlaVal

1150

1170

1190

FIG. 9 B

GTCTGGCTGGCCATCTGGCGGTGCTGTGCTTCTTCAGCGCCTCACCGTGCTCAC  
ValTrpLeuAlaIleTrpAlaValLeuCysPhePheSerSerAlaPheThrValLeuThr

1210

1230

1250

TTCCCTCATCGACCCGGCCCGCTTCCGCTACCCCGAGCGCCCCATCATCTCCTCTCCATG  
PheLeuIleAspProAlaArgPheArgTyrProGluArgProIleIlePheLeuSerMet

1270

1290

1310

TGCTACTGCGTCTACTCCGTGGGCTACCTCATCCGCCTCTCGCCGGCGCCGAGAGCATIC  
CysTyrCysValTyrSerValGlyTyrLeuIleArgLeuPheAlaGlyAlaGluSerIle

1330

1350

1370

GCCTGCGACCGGGACAGCGGCCAGCTCTATGTCATCCAGGAGGGACTGGAGAGCACCGGC  
AlaCysAspArgAspSerGlyGlnLeuTyrValIleGlnGluGlyLeuGluSerThrGly

1390

1410

1430

TGCACGCTGGTCTTCCTGGCCTACTACTTCGGCATGGCCAGCTCGCTGTGGTGGTG  
CysThrLeuValPheLeuValLeuTyrTyrPheGlyMetAlaSerSerLeuTrpTrpVal

1450

1470

1490

GTCCTCACGCTCACCTGGTTCTGGCCGCCGGCAAGAAGTGGGCCACGAGGCCATCGAA  
ValLeuThrLeuThrTrpPheLeuAlaAlaGlyLysLysTrpGlyHisGluAlaIleGlu

1510

1530

1550

GCCAACAGCAGCTACTCCACCTGGCAGCCTGGCCATCCGGCGGTGAAGACCATCCTG  
AlaAsnSerSerTyrPheHisLeuAlaAlaTrpAlaIleProAlaValLysThrIleLeu

1570

1590

1610

ATCCTGGTCATGCGCAGGGTGGCGGGGGACGAGCTCACCGGGGTCTGCTACGTGGCAGC  
IleLeuValMetArgArgValAlaGlyAspGluLeuThrGlyValCysTyrValGlySer

1630

1650

1670

ATGGACGTCAACGCGCTCACCGGCTTCGTGCTATTCCCCTGGCCTGCTACCTGGTCATC  
MetAspValAsnAlaLeuThrGlyPheValLeuIleProLeuAlaCysTyrLeuValIle

1690

1710

1730

FIG. 9 C

GGCACGTCTTCATCCTCTCGGGCTTGTGGCCCTGTTCCACATCCGGAGGGTGTGAAG  
 GlyThrSerPheIleLeuSerGlyPheValAlaLeuPheHisIleArgArgValMetLys

1750	1770	1790
ACGGGCGGCGAGAACACGGACAAGCTGGAGAAGCTCATGGTGCATCGGGCTCTCT		
ThrGlyGlyGluAsnThrAspLysLeuGluLysLeuMetValArgIleGlyLeuPheSer		
1810	1830	1850
GTGCTGTACACCGTGCCGGCACCTGTGTGATGCCCTGCTACTTTACGAACGCCCTAAC		
ValLeuTyrThrValProAlaThrCysValIleAlaCysTyrPheTyrGluArgLeuAsn		
1870	1890	1910
ATGGATTACTGGAAGATCCTGGCGGCGCAGCACAAAGTGCAAAATGAACAAACCAGACTAAA		
MetAspTyrTrpLysIleLeuAlaAlaGlnHisLysCysLysMetAsnAsnGlnThrLys		
1930	1950	1970
ACGCTGGACTGCCTGATGGCCGCCTCCATCCCCGCCGTGGAGATCTCATGGTGAAGATC		
ThrLeuAspCysLeuMetAlaAlaSerIleProAlaValGluIlePheMetValLysIle		
1990	2010	2030
TTTATGCTGCTGGTGGTGGGGATCACCAAGCGGGATGTGGATTGGACCTCCAAGACTCTG		
PheMetLeuLeuValValGlyIleThrSerGlyMetTrpIleTrpThrSerLysThrLeu		
2050	2070	2090
CAGTCCTGGCAGCAGGTGTGCAGCCGTAGGTTAAAGAAGAAGAGCCGGAGAAAACCGGCC		
GlnSerTrpGlnGlnValCysSerArgArgLeuLysLysSerArgArgLysProAla		
2110	2130	2150
AGCGTGATCACCAAGCGGTGGGATTACAAAAAGCCCAGCATCCCCAGAAAACCTACCCAC		
SerValIleThrSerGlyGlyIleTyrLysLysAlaGlnHisProGlnLysThrHisHis		
2170	2190	2210
GGGAAATATGAGATCCCTGCCAGTCGCCACCTGCGTGTGAACAGGGCTGGAGGGAGG		
GlyLysTyrGluIleProAlaGlnSerProThrCysValEnd		
2230	2250	2270

**FIG. 9 D**

GCACAGGGGCGCCCGGAGCTAAGATGTGGTCTTTCTTGGTTGTAAAACTTCT  
2290 2310 2330  
TCTTCTTTTTTTTATAAAAGCAAAAGAGAAATACATAAAAAGTGTACCCCTG  
2350 2370 2390  
AAATTCAAGGATGCTGTGATACACTGAAAGGAAAAATGTACTAAAGGGTTGTTGTT  
2410 2430 2450  
TTGGTTTCCAGCGAAGGGAAGCTCCTCCAGTGAAGTAGCCTCTGTGTAACAAATTGTT  
2470 2490 2510  
GGTAAAGTAGTTGATTCAGCCCTCAGAAGAAAACCTTTGTTAGAGCCCTCCSTAAATAT  
2530 2550 2570  
ACATCTGTGTATTCAGTTGGCTTGCTACCCATTACAAATAAGAGGACAGATAACTGC  
2590 2610 2630  
TTTGCAAATTCAAGAGCCTCCCTGGGTTAACAAATGAGCCATCCCCAGGGCCCACCCCC  
2650 2670 2690  
AGGAAGGCCACAGTGCTGGCGGCATCCCTGCAGAGGAAAGACAGGACCCGGGGCCGCC  
2710 2730 2750  
TCACACCCCCAGTGGATTGGAGTTGCTTAAATAGACTCCGGCCTCACCAATAGTCTCT  
2770 2790 2810  
CTGCAAGACAGAAACCTCCATCAAACCTCACATTGTGAACCTAAACGATGTGCAATACA  
2830 2850 2870  
TTTTTTCTTTCTTGAAAATAAAAGAGAAACAAGTATTTGCTATATATAAGACAG  
2890 2910 2930

FIG. 9 E

ACAAAAGAAATCTCCTAACAAAAGAACTAAGAGGCCAGCCCTCAGAAACCCTCAGTGC  
2950 2970 2990  
TACATTTGTGGCTTTAATGGAAACCAAGCCAATGTTAGACGTTGGACTGATTG  
3010 3030 3050  
TGGAAAGGAGGGGGGAAGAGGGAGAAGGATCATTCAAAAGTTACCCAAAGGGCTTATTGA  
3070 3090 3110  
CTCTTCTATTGTTAACAAATGATTCCACAAACAGATCAGGAAGCACTAGGTTGGCAG  
3130 3150 3170  
AGACACTTGCTAGTGTATTCTCTTCACAGTGCAGGAAAGAGTGGTTCTGCGTGTGT  
3190 3210 3230  
ATATTGTAATATATGATATTTCATGCTCCACTATTTATTAAAAATAAAATATGTTC  
3250  
TTTAGTTGCTGCT

FIG. 9 F

Location of SNPs/Amino Acid Changes/Domain within the Transcript of Gene 454

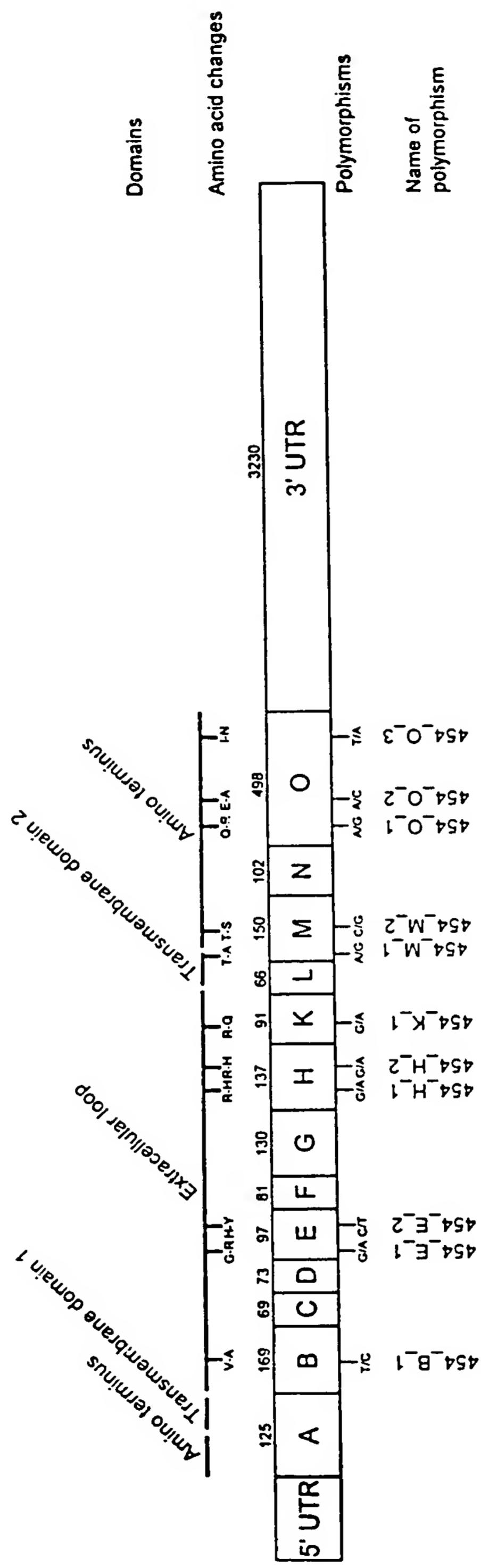


FIG. 10

Chr. 12 Case(Asthma)/Control: Alleles

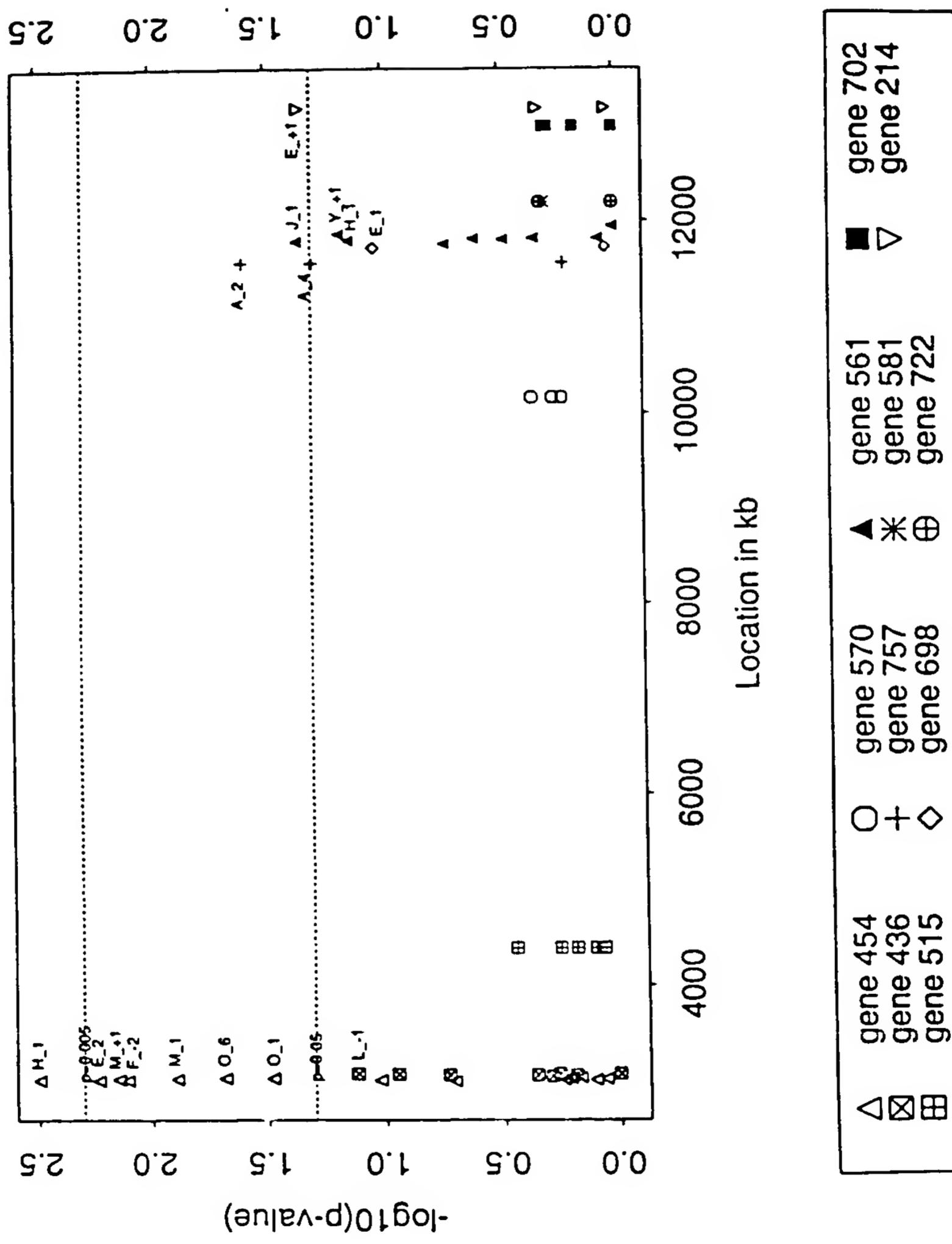
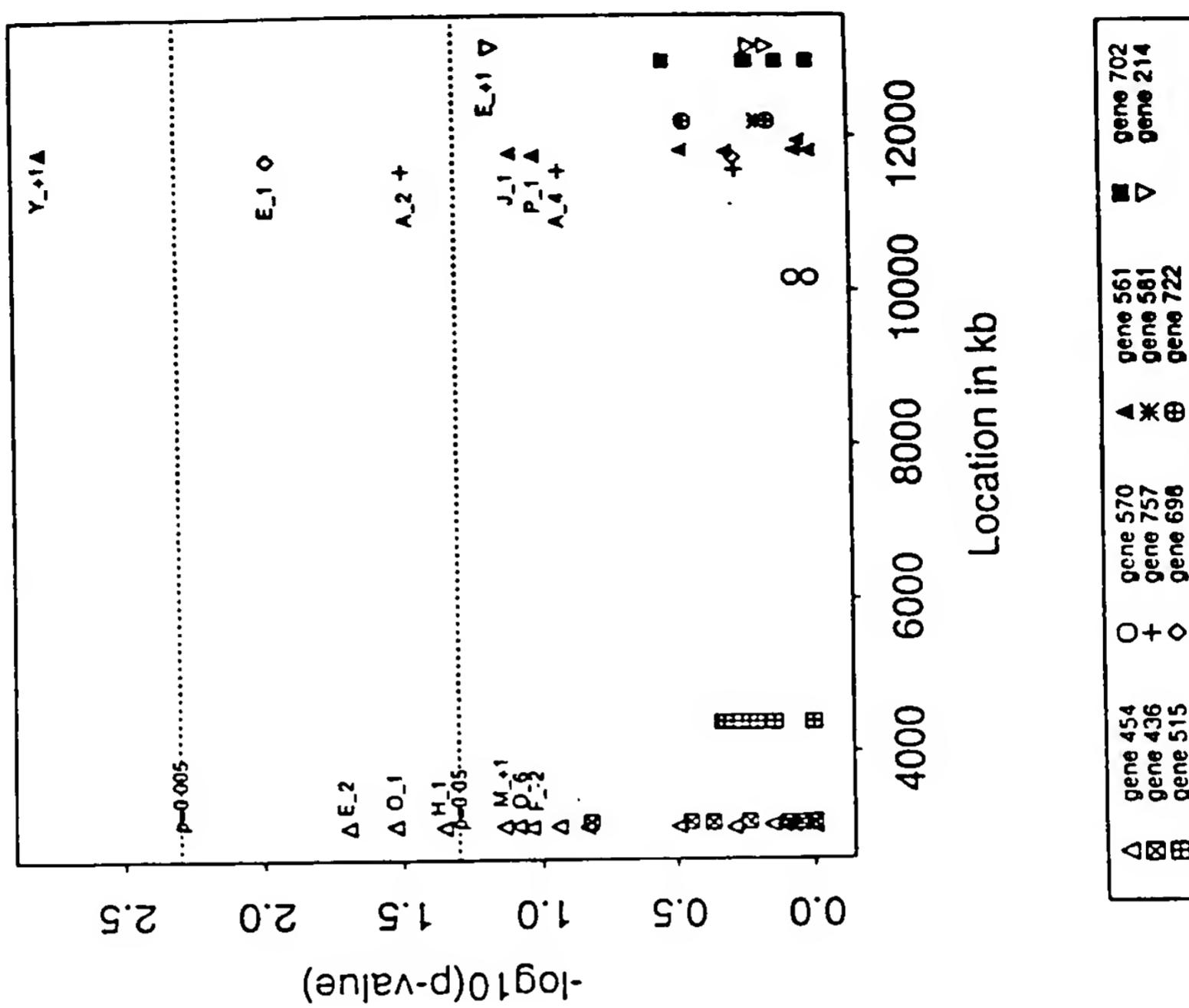
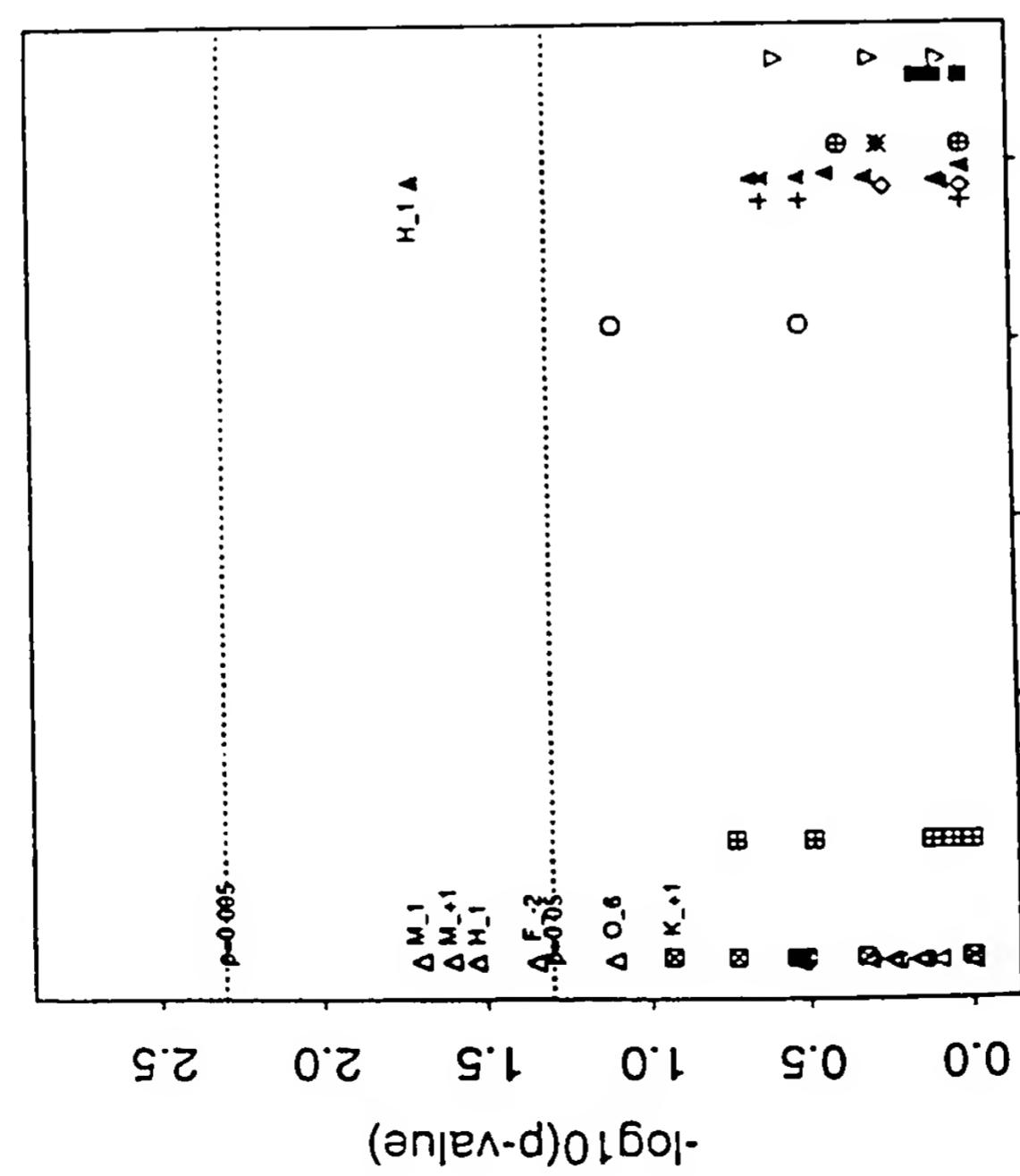


FIG. 11

Chr. 12 Case(Asthma)/Control: Alleles

US

UK



$\Delta$	gene 454
$\otimes$	gene 436
$\blacksquare$	gene 515
$\circ$	gene 570
$\oplus$	gene 757
$\times$	gene 561
$\diamond$	gene 696
$\blacksquare$	gene 702
$\triangledown$	gene 214
$\blacksquare$	gene 722

FIG. 12

Chr. 12 Case(BHR (PC<sub>20</sub> <= 16 mg/ml) & Asthma)/Control: Alleles

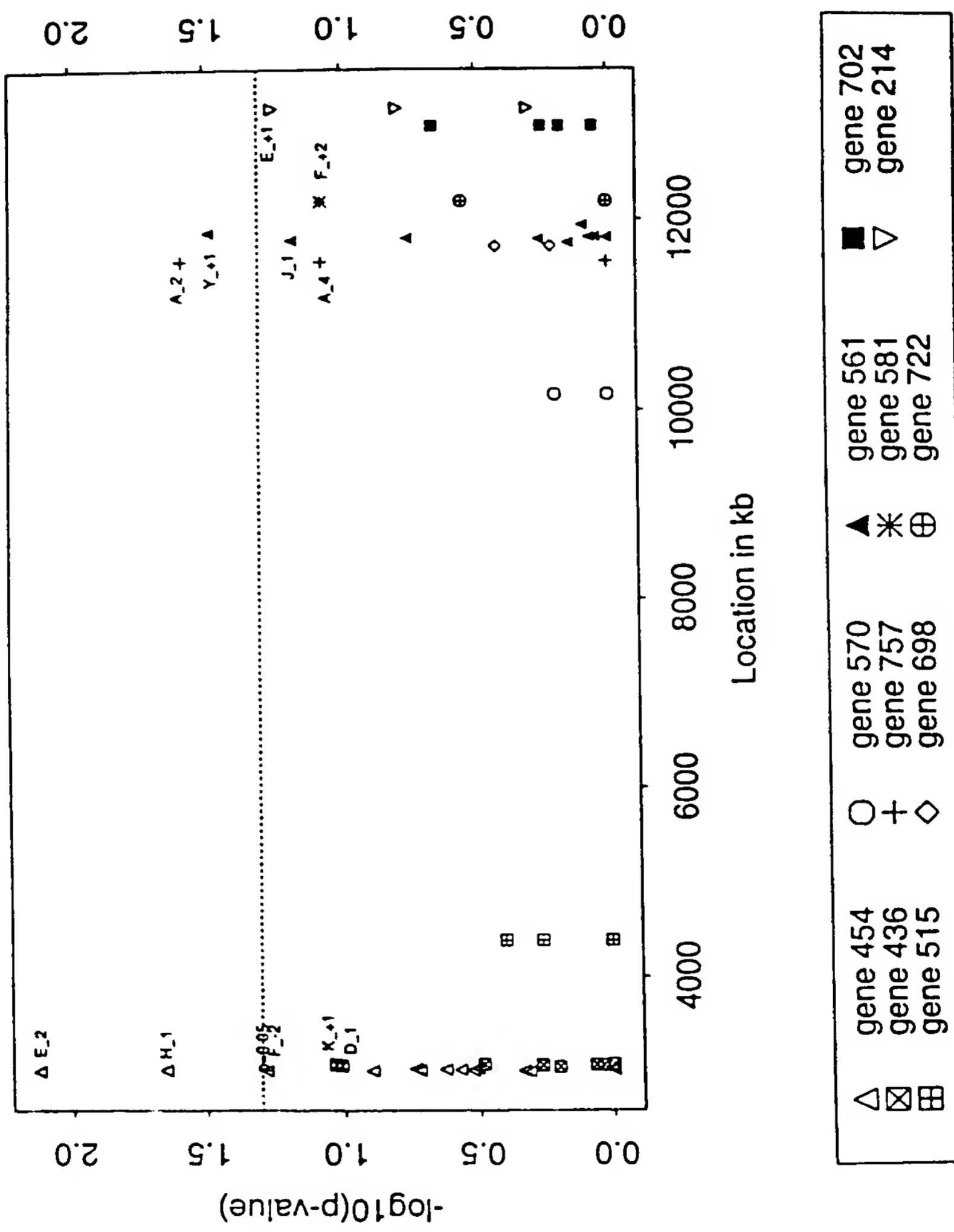


FIG. 13

Chr. 12 Case(BHR (PC<sub>20</sub> <= 16 mg/ml) & Asthma)/Control: Alleles

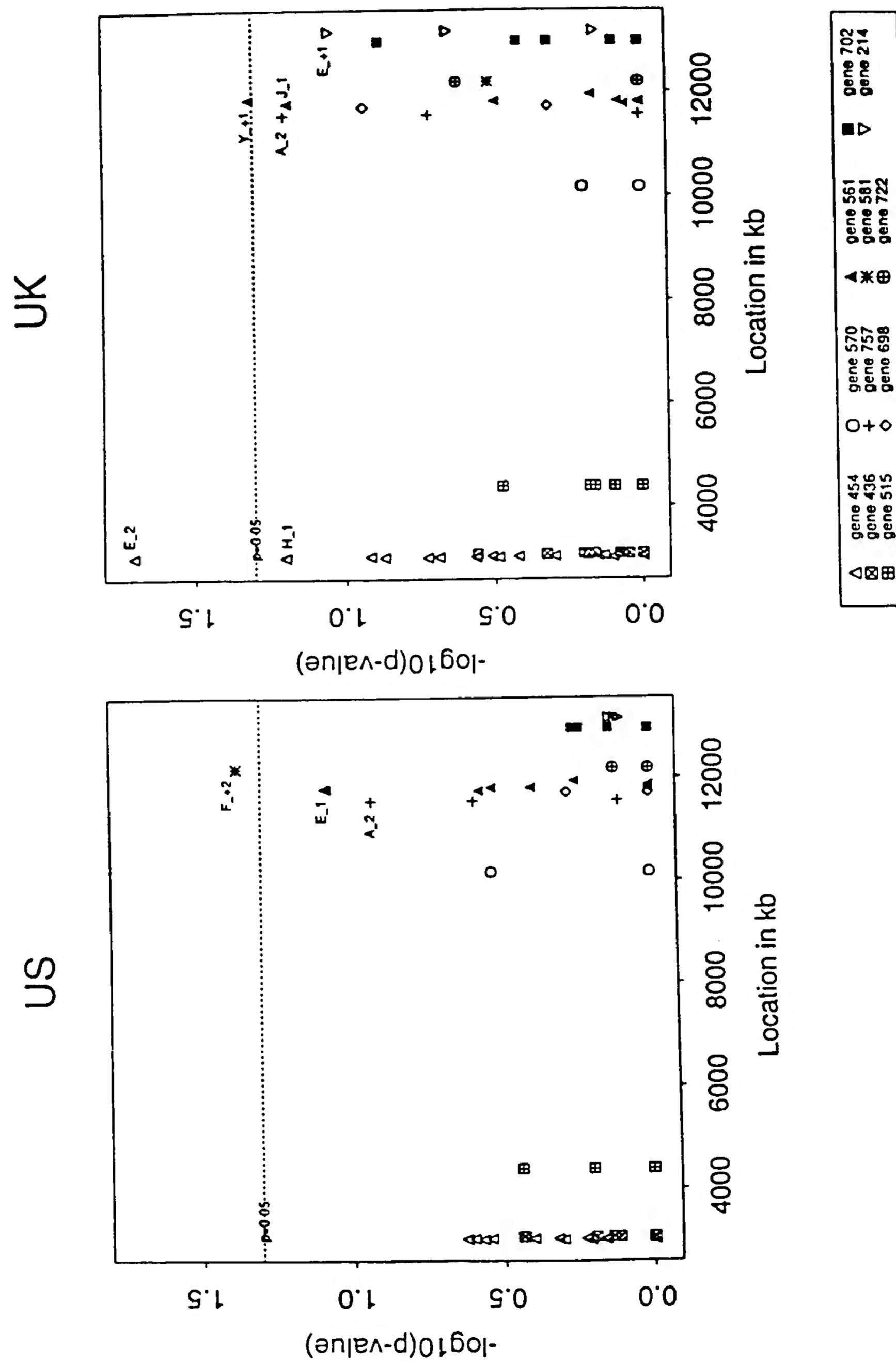


FIG. 14

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

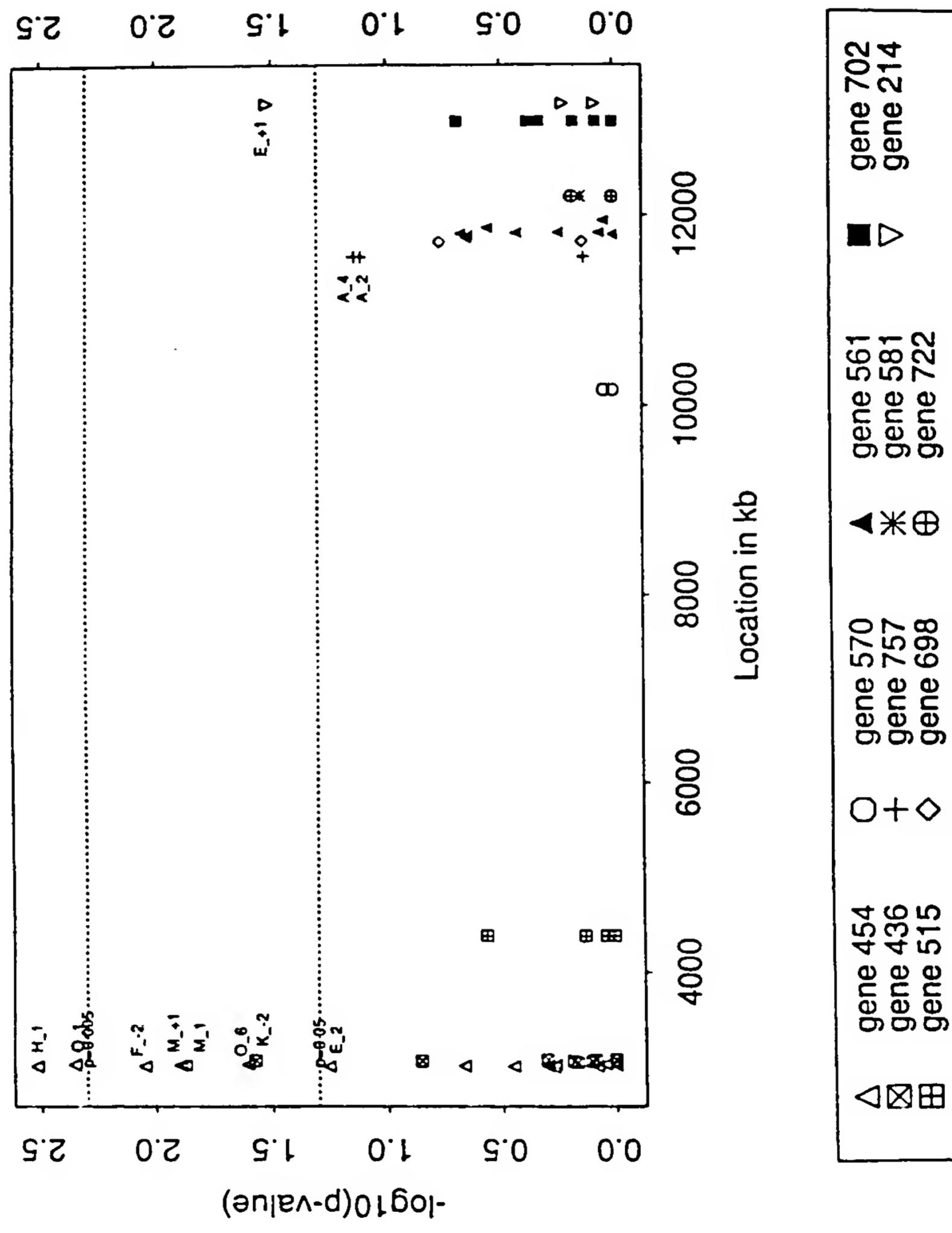
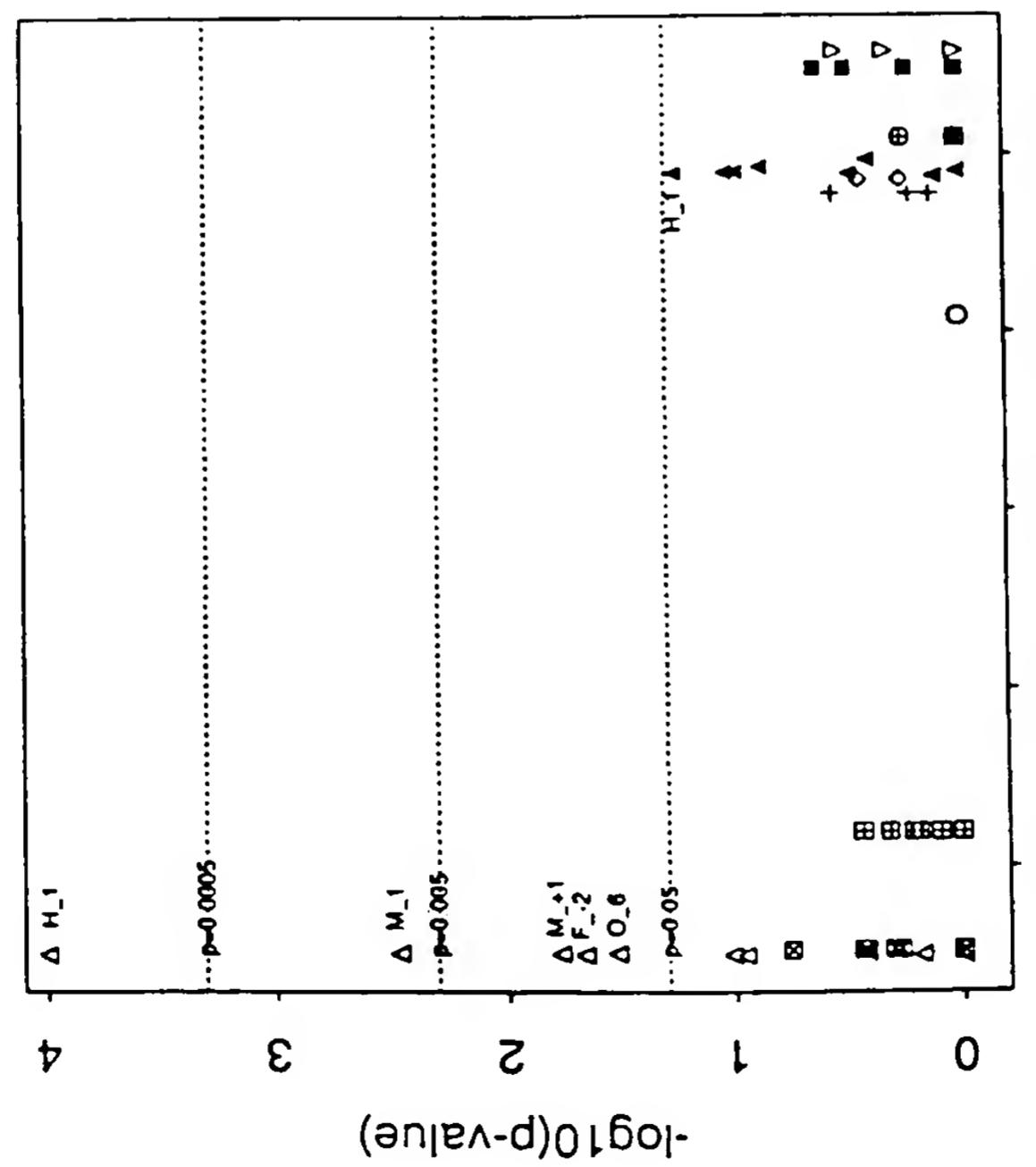


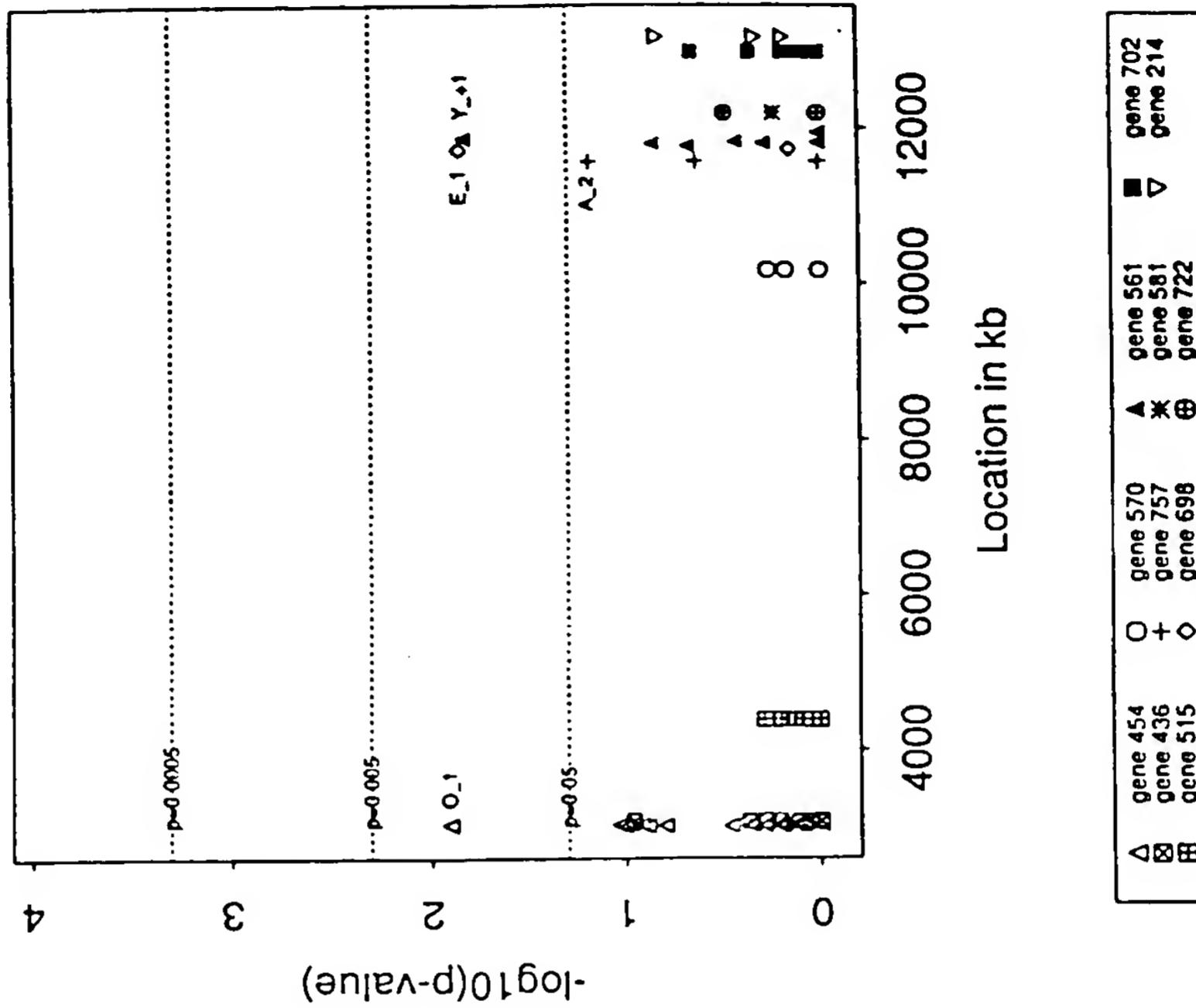
FIG. 15

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

US



UK



$\Delta$ gene 454	O gene 570	$\blacktriangle$ gene 561	$\blacksquare$ gene 702
$\square$ gene 436	+	$\times$ gene 581	$\triangledown$ gene 214
$\blacksquare$ gene 515	$\diamond$	$\oplus$ gene 698	$\oplus$ gene 722

FIG. 16

Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles

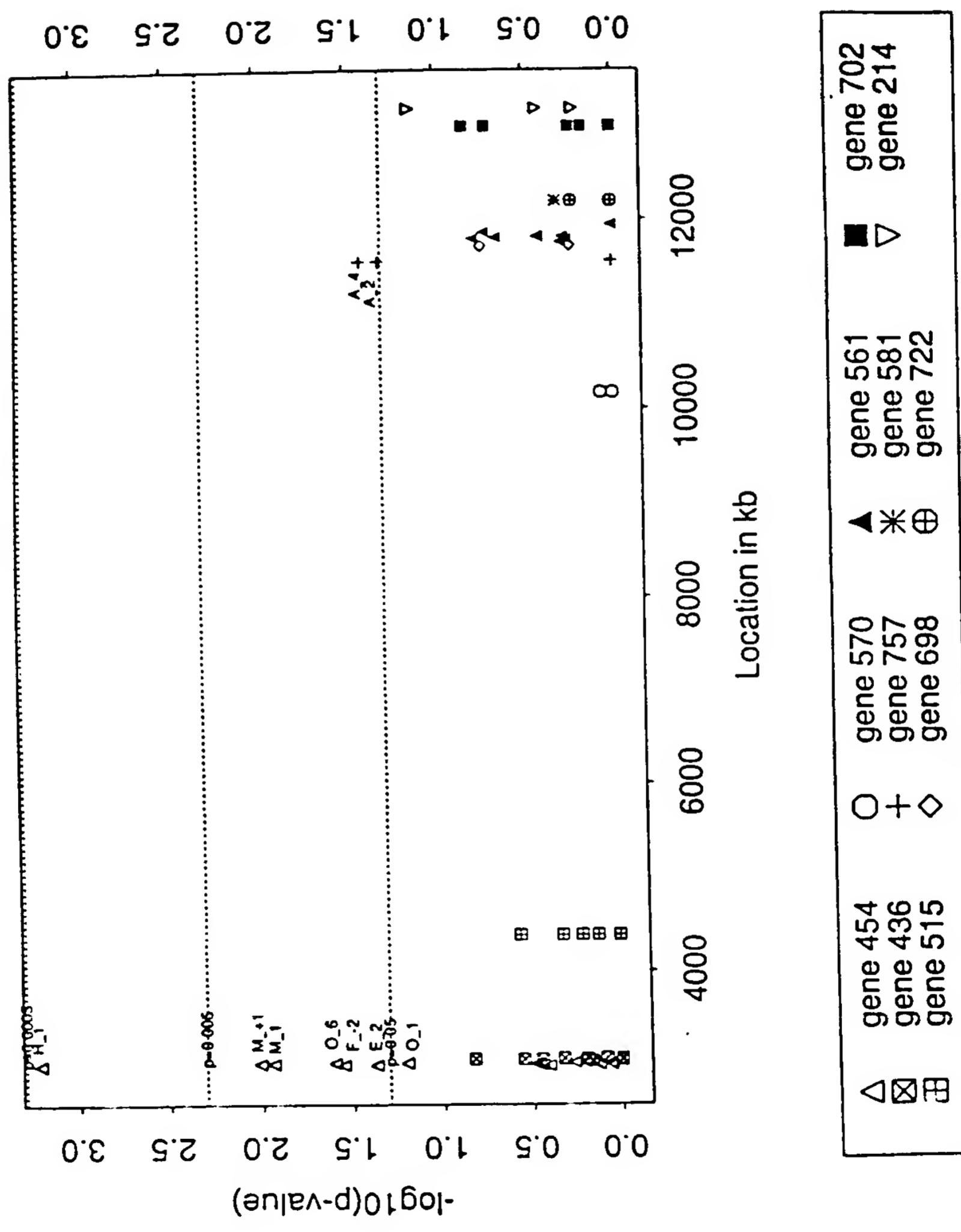


FIG. 17

Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles

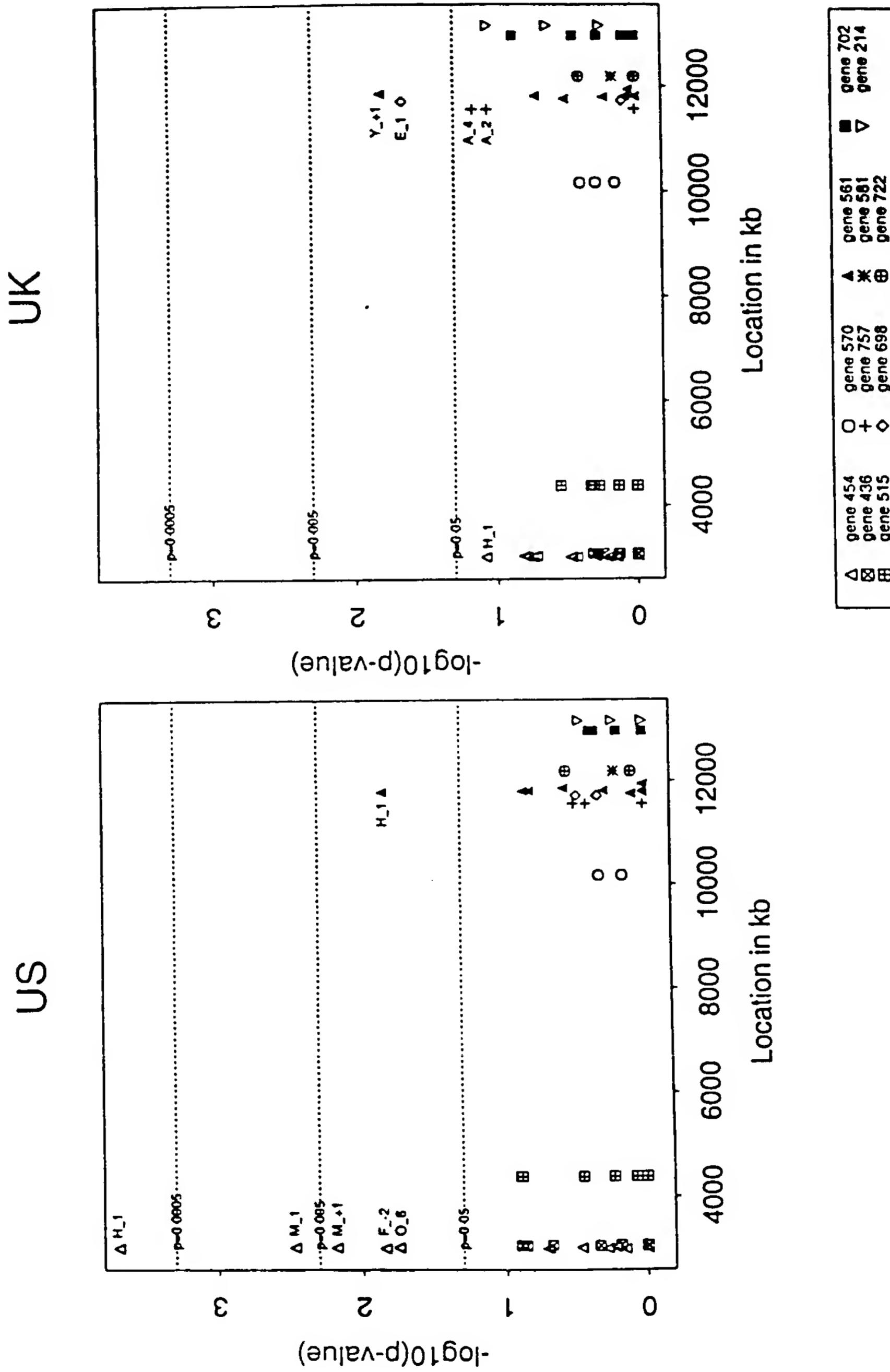


FIG. 18

Chr. 12 Case(Asthma)/Control: Haplotype

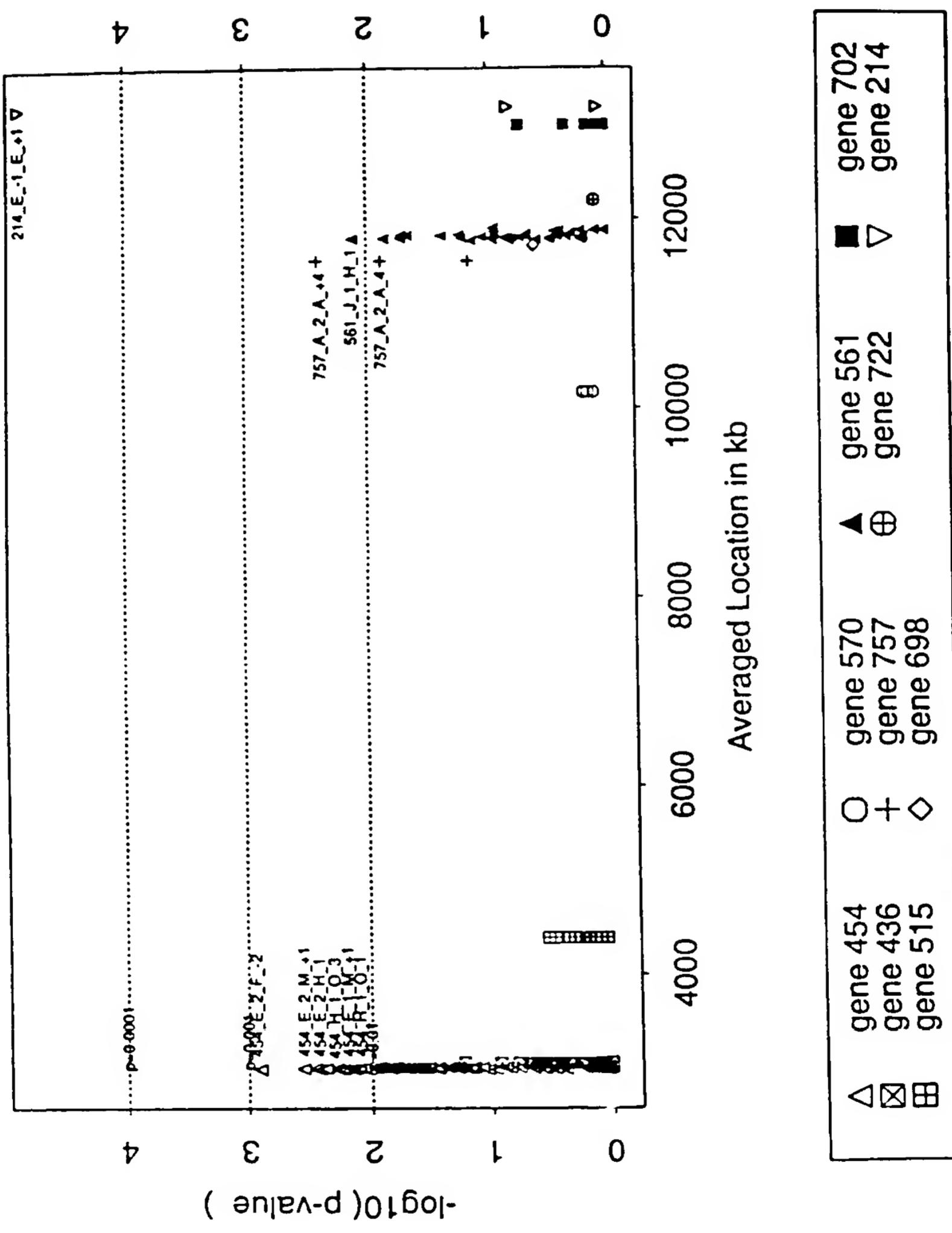


FIG. 19

Chr. 12 Case(Asthma)/Control: Haplotype

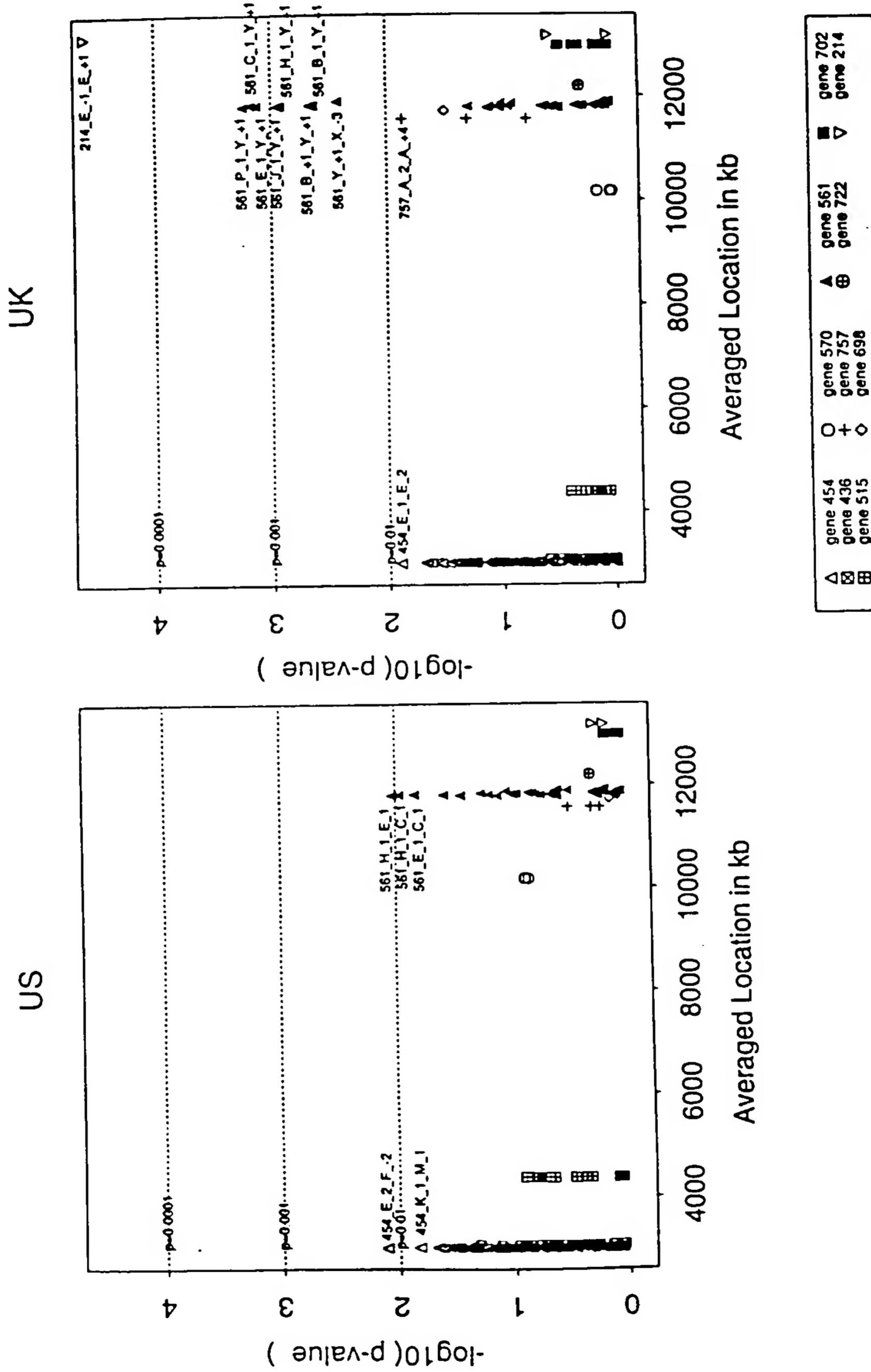


FIG. 20

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Haplotype

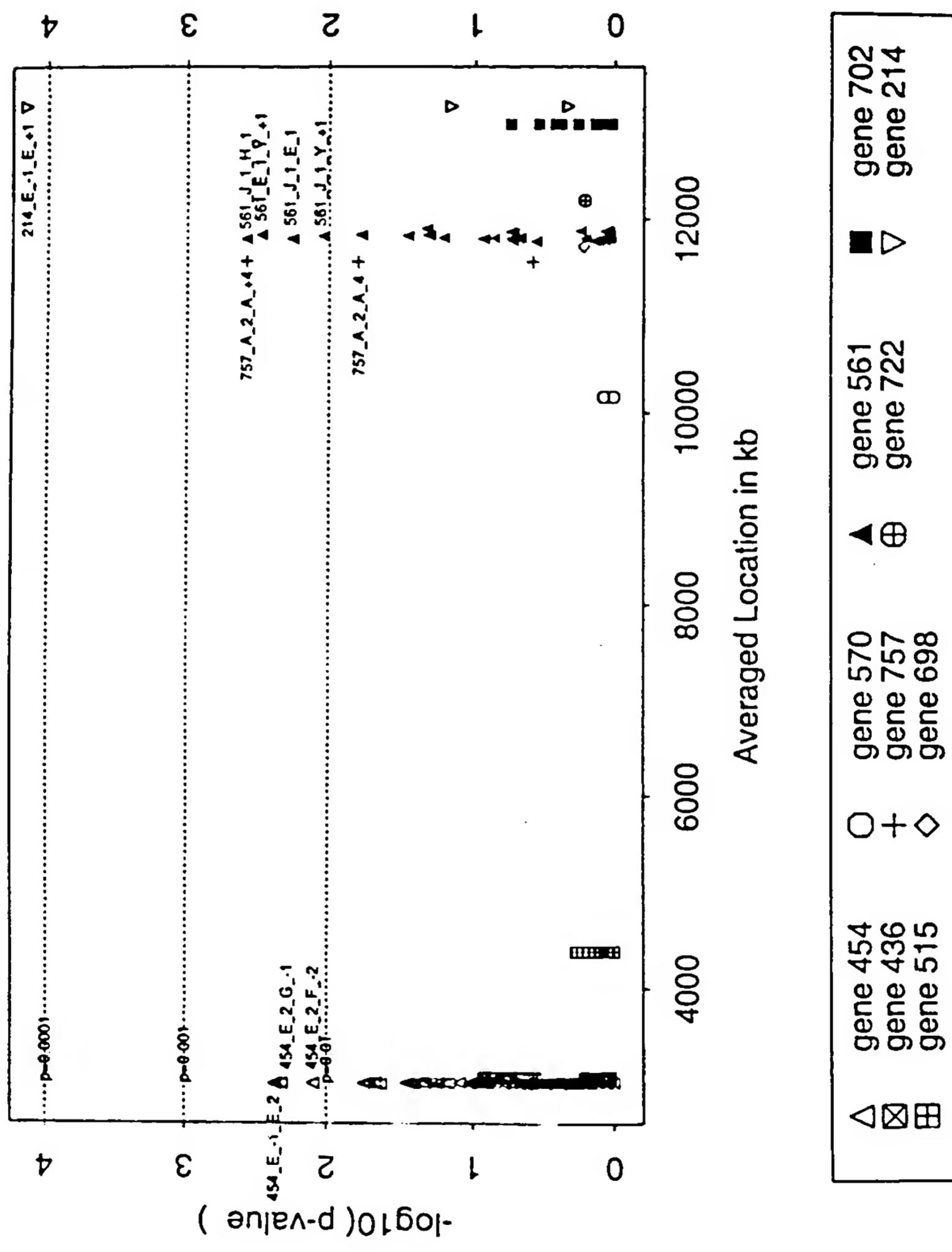


FIG. 21

Chr. 12 Case(BHR (PC<sub>20</sub> <= 16 mg/ml) & Asthma)/Control: Haplotype

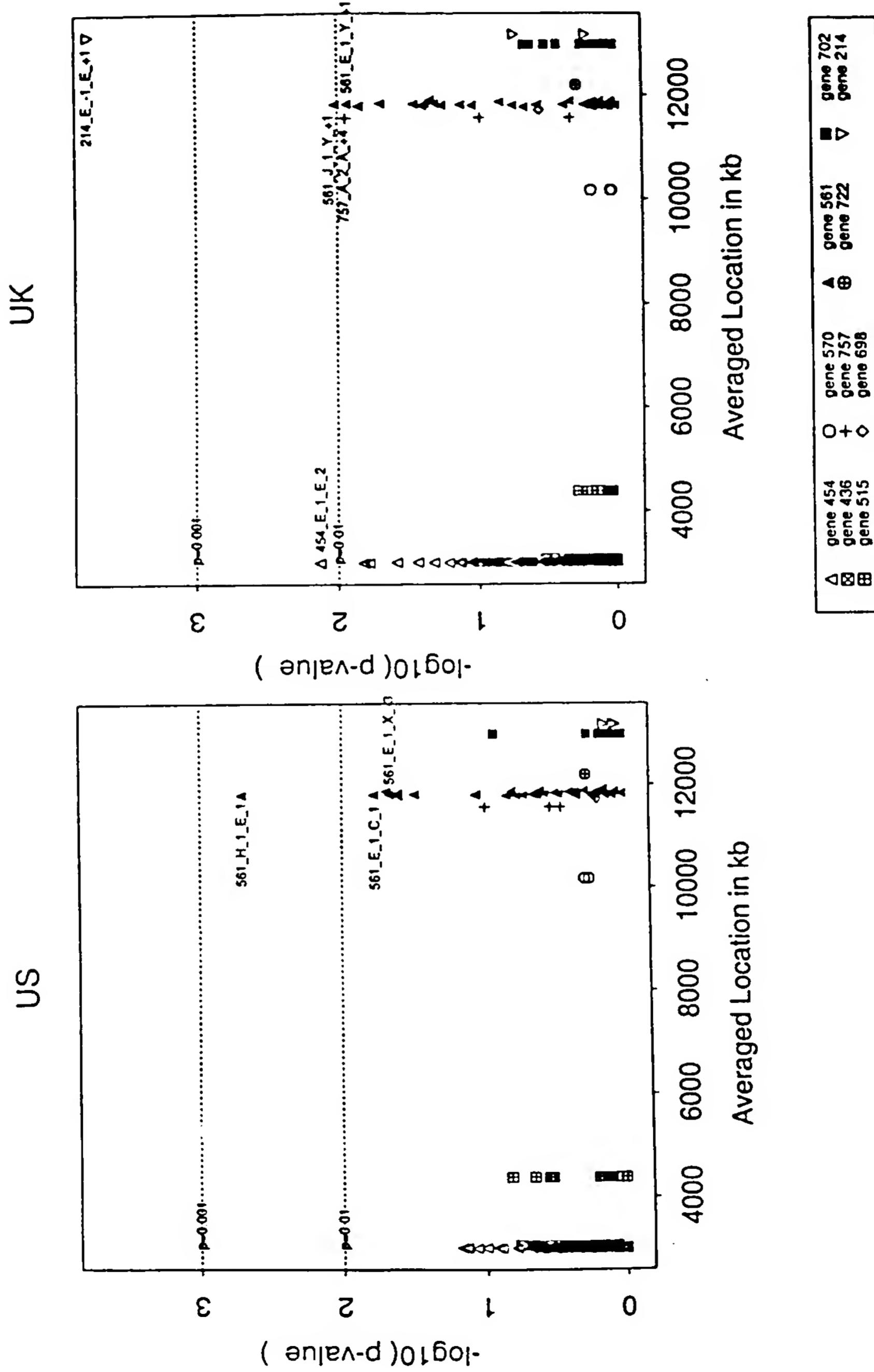
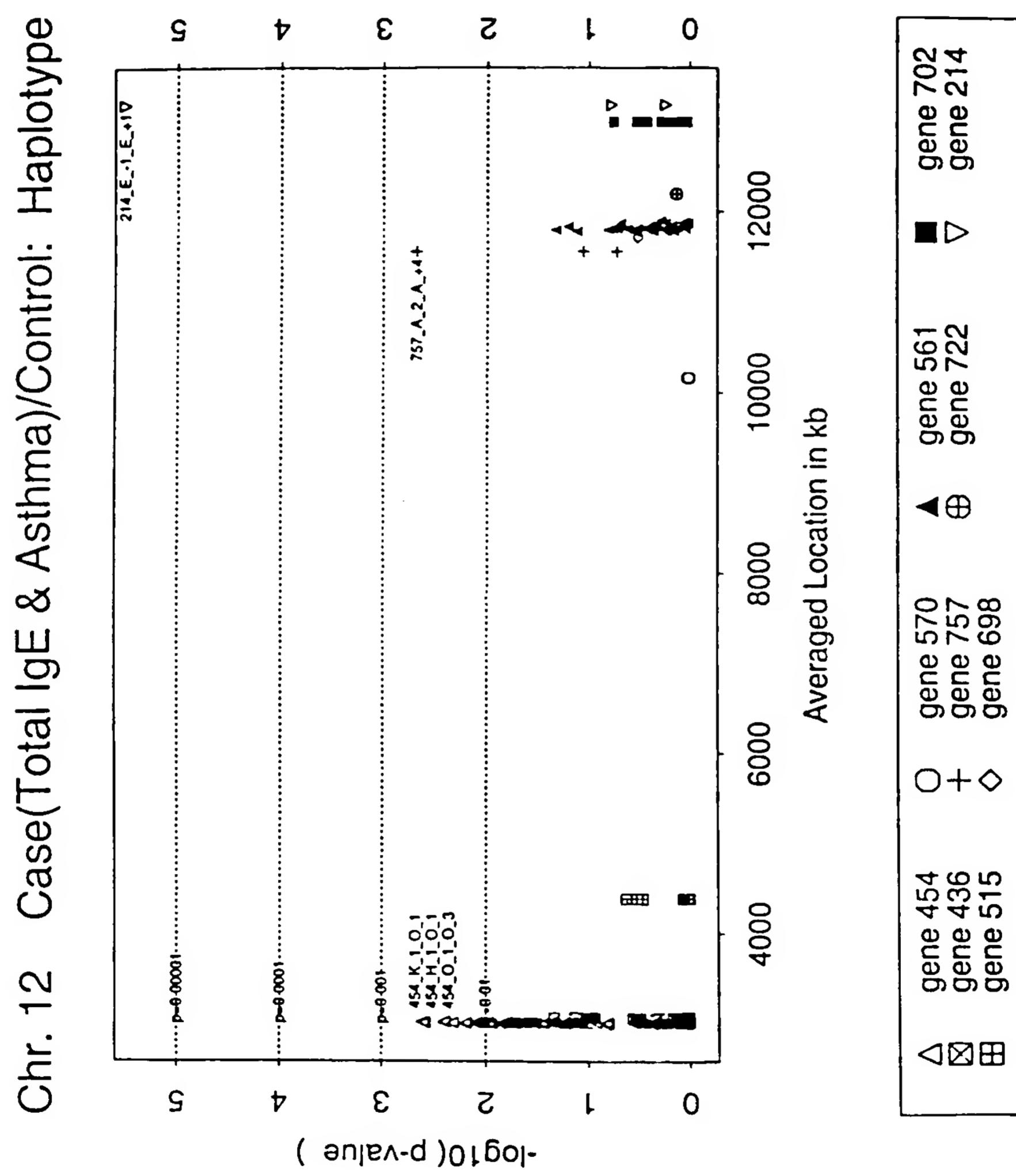


FIG. 22

FIG. 23



Chr. 12 Case(Total IgE & Asthma)/Control: Haplotype

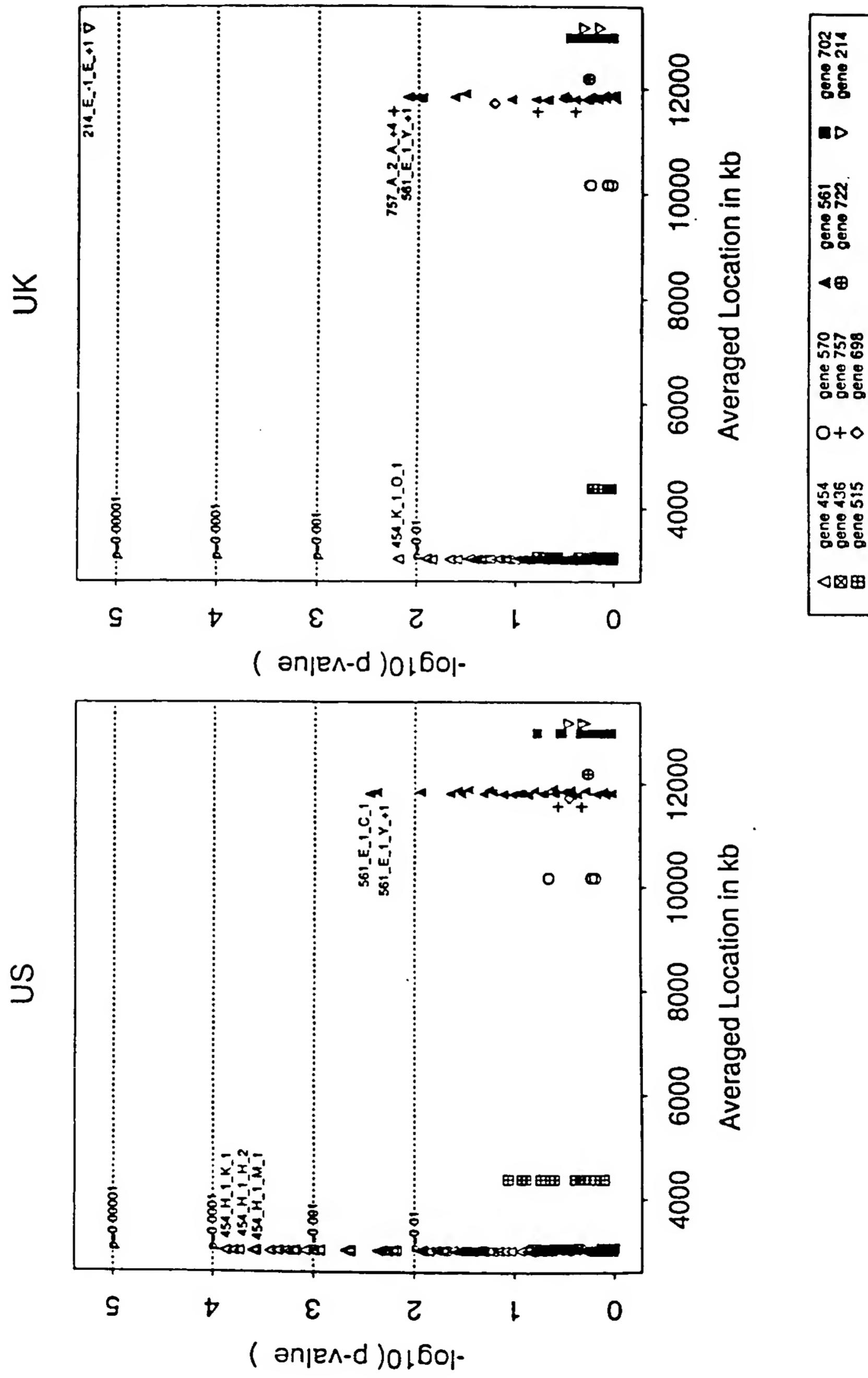


FIG. 24

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

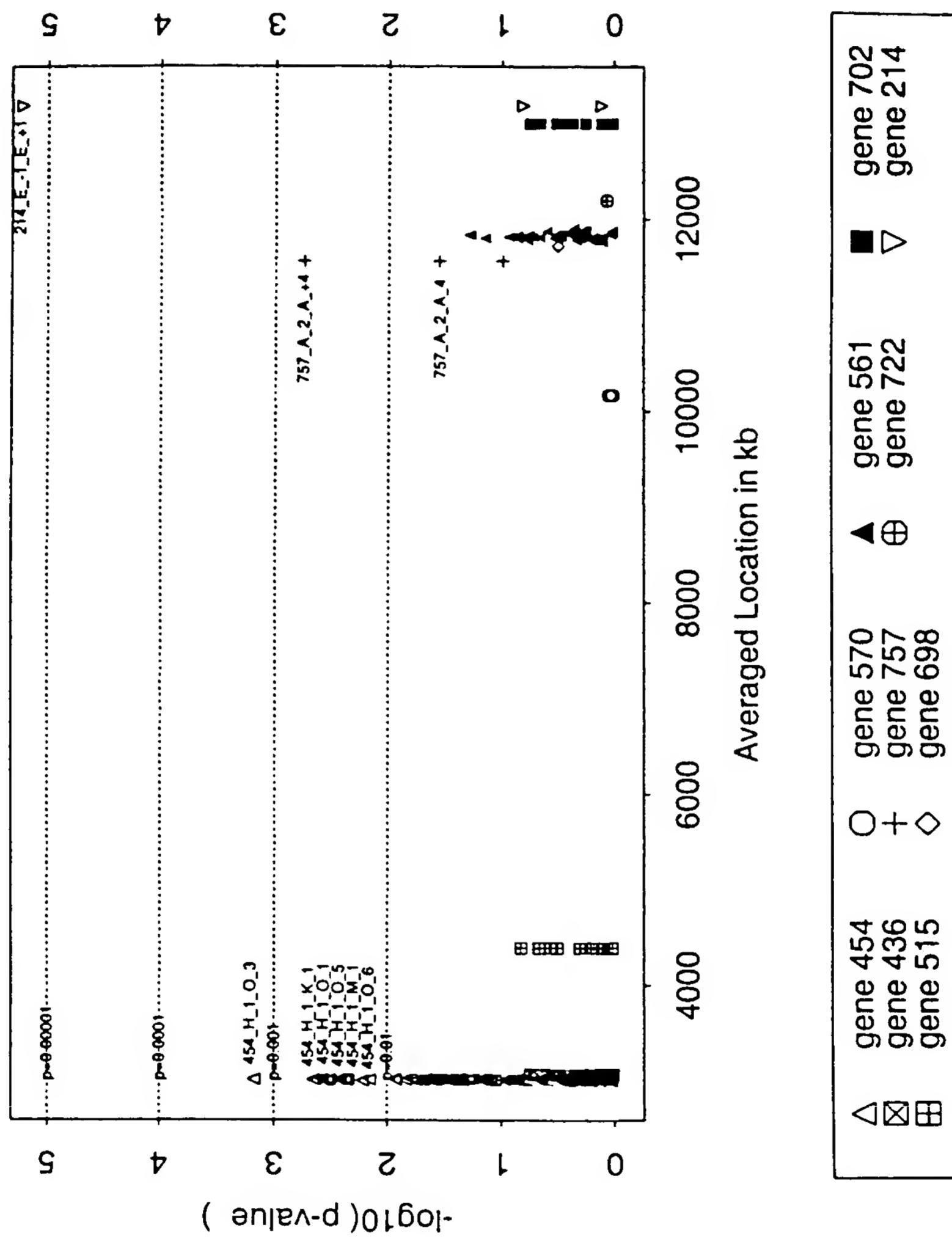


FIG. 25

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

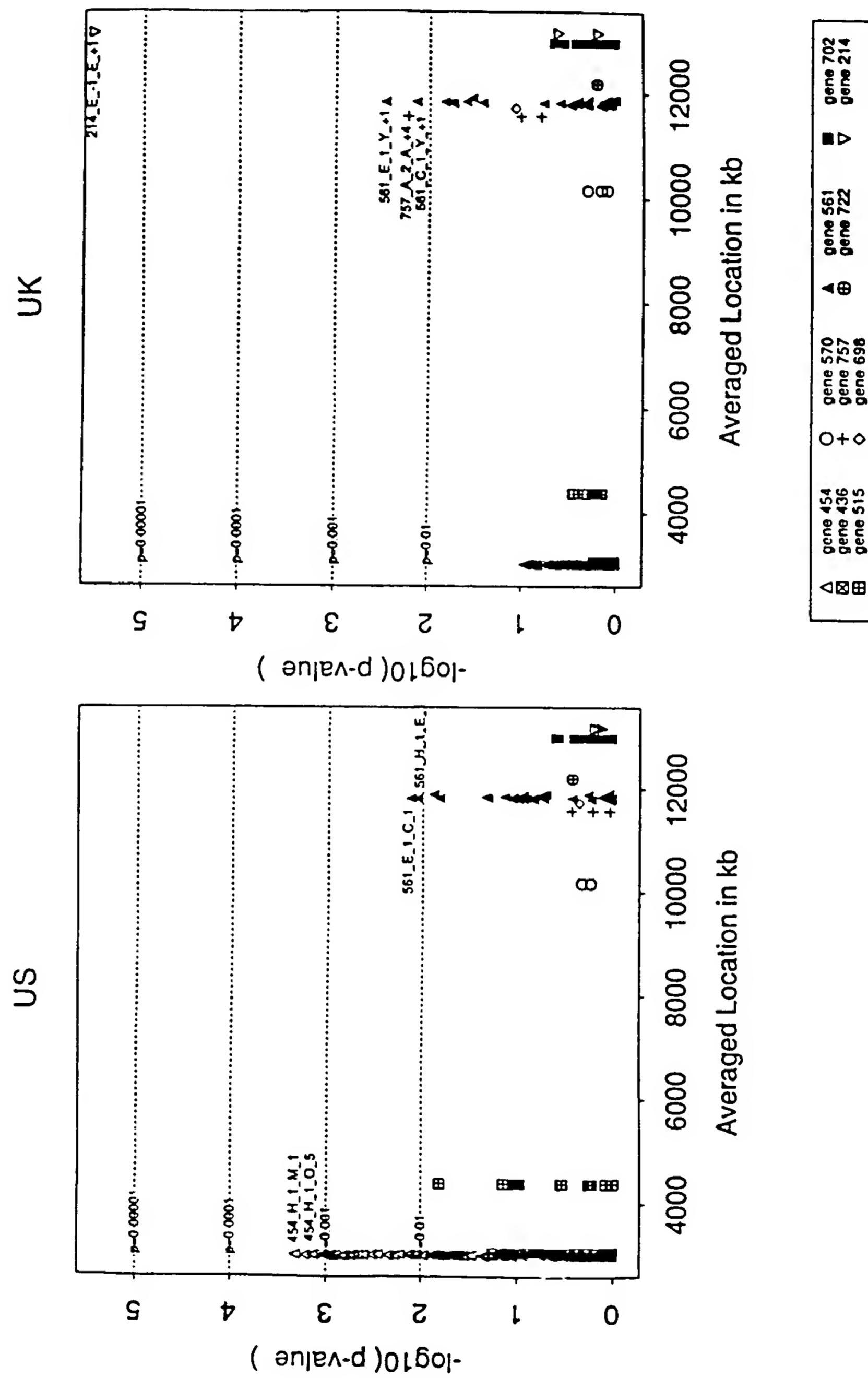


FIG. 26

10                   30                   50  
CTTGGAAATGACCCGCCACACCTGAAGCCTGCAGGTGCTGAGGCCACATTGATCAGACC  
  
70                   90                   110  
CAAGCTTGAGACCGCTGGGAAATTCCCACTTCCCTCCTGAGACCAGGAACTCAG  
  
130                  150                  170  
CAGAGAAACTTGTGGAAAATGAACGTGAAGGATGCCACCCAGGGAGAGTATCTCCTGAGA  
  
190                  210                  230  
TCCCCATCATGCAGGCCTTCCCACAAGGGCCGGCAGCATGACAAGGTGAAGGCAGAGTAT  
  
250                  270                  290  
GTGCATCTCAACCAYCCGCTCACCCCTCGTGACCAGAGAGCGCGATTGGCCGTGAAGGAG  
  
310                  330                  350  
AAACACCAGCTCCAAGCCAAGCTGGAGAACCTAGAACAGGTCTGAAGCATATGCGAGAG  
MetArgGlu  
  
370                  390                  410  
GCGGCTGAACGGCGGCAGCAGCTGCAGTTGGAGCATGACCAGGCCCTGGCTGTTCTCAGT  
AlaAlaGluArgArgGlnGlnLeuGlnLeuGluHisAspGlnAlaLeuAlaValLeuSer  
  
430                  450                  470  
GCCAAGCAGCAGGAAATTGACCTTCTGCAGAAGTCCAAGGTTGAGAGAGCTGGAAGAGAAA  
AlaLysGlnGlnGluIleAspLeuLeuGlnLysSerLysValArgGluLeuGluGluLys  
  
490                  510                  530  
TGCCGGACTCAAAGTGAGCAGTTCAACCTGCTGTCCGGGACCTGGAGAAGTTCCGGCAG  
CysArgThrGlnSerGluGlnPheAsnLeuLeuSerArgAspLeuGluLysPheArgGln  
  
550                  570                  590  
CACGCTGGCAAGATTGACCTGCTGGGTGGCAGCGCGGTGGCCCCCTGGACATCTCCACG  
HisAlaGlyLysIleAspLeuLeuGlyGlySerAlaValAlaProLeuAspIleSerThr

FIG. 27 A

610                    630                    650  
GCC CCCCCAGCAAGCCTTCCCACAGTTCATGAATGGCCTAGCCACCTCCCTCGGCAAAGGT  
Ala Pro Ser Lys Pro Phe Pro Gln Phe Met Asn Gly Leu Ala Thr Ser Leu Gly Lys Gly

670                    690                    710  
CAGGAGAGCGCTATTGGAGGCAGCTCTGCGATCGGTGAATATATCCGGCCCTCCGCAG  
Gln Glu Ser Ala Ile Gly Gly Ser Ser Ala Ile Gly Glu Tyr Ile Arg Pro Leu Pro Gln

730                    750                    770  
CCTGGTGACAGGCCGGAGCCTCTGTCCGCCAAGCCCACCTTCCTGTCGAGATCCGGTAGC  
Pro Gly Asp Arg Pro Glu Pro Leu Ser Ala Lys Pro Thr Phe Leu Ser Arg Ser Gly Ser

790                    810                    830  
GCAAGATGCAGATCTGAGTCAGACATGGAGAATGAACGGAATTCCAATACCTCCAAGCAG  
Ala Arg Cys Arg Ser Glu Ser Asp Met Glu Asn Glu Arg Asn Ser Asn Thr Ser Lys Gln

850                    870                    890  
AGATACTCGGGGAAGGTCCACCTCTGTGTTGCCGCTATAGTTACAACCCCTTCGATGGA  
Arg Tyr Ser Gly Lys Val His Leu Cys Val Ala Arg Tyr Ser Tyr Asn Pro Phe Asp Gly

910                    930                    950  
CCGAACGAGAACCCCGAAGCTGAGCTGCCCTCACGGCGGGAAAATACCTCTACGTCTAT  
Pro Asn Glu Asn Pro Glu Ala Glu Leu Pro Leu Thr Ala Gly Lys Tyr Leu Tyr Val Tyr

970                    990                    1010  
GGAGACATGGATGAGGATGGGTTCTATGAAGGAGAGCTCCTCGATGCCAGAGGGGTCTG  
Gly Asp Met Asp Glu Asp Gly Phe Tyr Glu Gly Glu Leu Leu Asp Gly Gln Arg Gly Leu

1030                    1050                    1070  
GTGCCCTCCAACCTCGTGGACTTGTGCAGGACAACGAGTCGCGGTTGGCAAGCACGCTG  
Val Pro Ser Asn Phe Val Asp Phe Val Gln Asp Asr Glu Ser Arg Leu Ala Ser Thr Leu

1090                    1110                    1130  
GGGAACGAGCAGGATCAGAACTTCATCAACCATTCCGGCATCGGCCTGGAGGGAGAGCAC  
Gly Asn Glu Gln Asp Gln Asn Phe Ile Asn His Ser Gly Ile Gly Leu Glu Gly Glu His

1150                    1170                    1190  
ATCCTGGACCTCCACTCCCCAACCCACATAGATGCCGGCATCACCGACAACAGTGCCGGG

FIG. 27 B

IleLeuAspLeuHisSerProThrHisIleAspAlaGlyIleThrAspAsnSerAlaGly

1210

1230

1250

ACCCCTGGACGTGAACATCGACGACATCGGAGAAGACATCGTGCCTTACCCCTAGAAAAATC  
ThrLeuAspValAsnIleAspAspIleGlyGluAspIleValProTyrProArgLysIle

1270

1290

1310

ACCCCTCATCAAACAACACTGCCAAAAGTGTATTGTGGCTGGGAGCCCCCGGCGGTGCCA  
ThrLeuIleLysGlnLeuAlaLysSerValIleValGlyTrpGluProProAlaValPro

1330

1350

1370

CCAGGATGGGAAACGGTGAGCAGCTAACGTCTGGACAGGAGCACGGCATGAAC  
ProGlyTrpGlyThrValSerSerTyrAsnValLeuValAspLysGluThrArgMetAsn

1390

1410

1430

CTCACGCTGGGAGCAGAACTAAAGCCCTCATCGAGAAGCTAACATGGCAGCCTGCACC  
LeuThrLeuGlySerArgThrLysAlaLeuIleGluLysLeuAsnMetAlaAlaCysThr

1450

1470

1490

TACCGCATCTCCGTGCAGTGCAGTCACCAGCAGGGCAGCTGGATGAGCTGCAGTGCACG  
TyrArgIleSerValGlnCysValThrSerArgGlySerSerAspGluLeuGlnCysThr

1510

1530

1550

CTGCTGGTGGCAAGGACGTGGTGGTGGCCCCCTCCACCTGCAGGACAACATCACG  
LeuLeuValGlyLysAspValValValAlaProSerHisLeuArgValAspAsnIleThr

1570

1590

1610

CAGATCTCCGCCAGCTCTCCTGGCTACCCACCAACAGCAACTACAGCCACGTCTTC  
GlnIleSerAlaGlnLeuSerTrpLeuProThrAsnSerAsnTyrSerHisValIlePhe

1630

1650

1670

CTCAACGAGGAGGAGTTGACATCGTCAAGGCCGCCAGGTACAAGTACCAAGTCTTCAAT  
LeuAsnGluGluPheAspIleValLysAlaAlaArgTyrLysTyrGlnPhePheAsn

1690

1710

1730

CTCAGGCCAACATGGCCTATAAGGTGAAGGTTCTGGCAAACCCCACCAAGATGCCGTGG  
LeuArgProAsnMetAlaTyrLysValLysValLeuAlaLysProHisGlnMetProTrp

FIG. 27 C

1750

1770

1790

CAGCTCCGCTGGAGCAAAGGGAGAAGAAGGGAGGCCTTGTGGAGTTCTCACGTTGCCT  
GlnLeuProLeuGluGlnArgGluLysLysGluAlaPheValGluPheSerThrLeuPro

1810

1830

1850

GCAGGACCCCCAGCACCCCCACAAGATGTTACCGTCCAGGCTGGGTGACCCCCGCCACC  
AlaGlyProProAlaProProGlnAspValThrValGlnAlaGlyValThrProAlaThr

1870

1890

1910

ATCCGGGTCTCCTGGAGACCACCTGTGCTGACGCCACCAGCTGTCCAATGGCGCAAAC  
IleArgValSerTrpArgProProValLeuThrProThrGlyLeuSerAsnGlyAlaAsn

1930

1950

1970

GTTACCGGCTACGGCGTGTATGCCAAAGGGCAGAGGGTGGCTGAAGTCATCTTCCCCACG  
ValThrGlyTyrGlyValTyrAlaLysGlyGlnArgValAlaGluValIlePheProThr

1990

2010

2030

GCAGACAGCACGGCCGTGGAGCTTGTGCGGCTGCGAGCCTGGAGGCCAACGGCGTGACC  
AlaAspSerThrAlaValGluLeuValArgLeuArgSerLeuGluAlaLysGlyValThr

2050

2070

2090

GTGCGGACCCCTCTCCGCCAACGGCGAGTCCGTGGACTCTGCAGTTGCTGCCGTTCCCCC  
ValArgThrLeuSerAlaGlnGlyGluSerValAspSerAlaValAlaAlaValProPro

2110

2130

2150

GAGCTCCTGGTGCCTCCTACCCCCCACCGAGACCTGCACCCCAATCAAAGCCATTAGCA  
GluLeuLeuValProProThrProHisProArgProAlaProGlnSerLysProLeuAla

2170

2190

2210

AGTTCTGGAGTCCCCGAAACCAAAGACGAGCACCTGGGTCCCCACGCCAGGATGGATGAG  
SerSerGlyValProGluThrLysAspGluHisLeuGlyProHisAlaArgMetAspGlu

2230

2250

2270

GCCTGGGAGCAGAGCCGTGCACCTGGCCCTGTGCATGGCACATGCTGGAGGCCGCCGTG  
AlaTrpGluGlnSerArgAlaProGlyProValHisGlyHisMetLeuGluProProVal

2290

2310

2330

GGCCCCGGAAGGCGGTGCGCCCTCACCCAGCCGCATCCTGCCGCAGCCACAGGGCACCCCG

GlyProGlyArgArgSerProSerProSerArgIleLeuProGlnProGlnGlyThrPro

2350

2370

2390

GTGTCCACCACCGTCGCCAAGGCCATGGCCCGGGAGGCCGCAGAGGGTGGCGAGAGC  
ValSerThrThrValAlaLysAlaMetAlaArgGluAlaAlaGlnArgValAlaGluSer

2410

2430

2450

AGCAGGTTAGAGAAAAGGAGCGTCTTCCTAGAGAGAACGAGCGGGGGCAGTACGCCGCC  
SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla

2470

2490

2510

TCAGACGAGGAGGACGCCTATGACTCTCCAGACTTCAAGAGGAGGGGCCCTCGGTGGAC  
SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp

2530

2550

2570

GACTTCCTGAAAGGCTCTGAACCTGGCAAGCAGCCGACTGTTGCCATGGAGACGAGTAC  
AspPheLeuLysGlySerGluLeuGlyLysGlnProHisCysCysHisGlyAspGluTyr

2590

2610

2630

CACACAGAGAGCAGCCGGGGTCTGACCTCTCAGACATCATGGAGGAGGACGAGGAGGAG  
HisThrGluSerSerArgGlySerAspLeuSerAspIleMetGluGluAspGluGlu

2650

2670

2690

CTGTATTCTGAAATGCAGCTGGAAGATGGGGGAAGGAGGGGCGGCCAGCGGCACGTCCCAC  
LeuTyrSerGluMetGlnLeuGluAspGlyGlyArgArgArgProSerGlyThrSerHis

2710

2730

2750

AATGCCCTCAAGATTAGGAAACCCAGCCTCTGCAGGACGGTGGATCACATGGGCCGG  
AsnAlaLeuLysIleLeuGlyAsnProAlaSerAlaGlyArgValAspHisMetGlyArg

2770

2790

2810

AGGTTCCCCGTGGCAGCGCTGGCCTCAGAGGTCCGGCCGTGACAGTCCCACATCCATC  
ArgPheProArgGlySerAlaGlyProGlnArgSerArgProValThrValProSerIle

2830

2850

2870

GACGATTACGGCGAGACCGCCTTCTCCAGACTTCTATGAAGAGTCAGAAACTGACCCCT  
AspAspTyrGlyArgAspArgLeuSerProAspPheTyrGluGluSerGluThrAspPro

2890                    2910                    2930  
GGTGCCGAAGAGCTCCGGCCGGATCTTGTGGCTCTTTGACTACGACCCGCTCACC  
GlyAlaGluGluLeuProAlaArgIlePheValAlaLeuPheAspTyrAspProLeuThr

2950                    2970                    2990  
ATGTCCCCAAACCCAGATGCTGCAGAGGAGGAGCTCCCTTAAAGAAGGCCAGATCATC  
MetSerProAsnProAspAlaAlaGluGluLeuProPheLysGluGlyGlnIleIle

3010                    3030                    3050  
AAGGTTTATGGTATAAAGACGCTGATGGATTCTACCGTGGGAAACCTGTGCCCGGCTT  
LysValTyrGlyAspLysAspAlaAspGlyPheTyrArgGlyGluThrCysAlaArgLeu

3070                    3090                    3110  
GGCCTTATTCTTGTAACATGGTCTCTGAGATACAAGCAGATGATGAGGAGATGGAT  
GlyLeuIleProCysAsnMetValSerGluIleGlnAlaAspAspGluGluMetMetAsp

3130                    3150                    3170  
CAGCTCTTAGACAGGGCTTCTCCCTCTGAATACACCTGTGGAGAAAATAGAGAGAAC  
GlnLeuLeuArgGlnGlyPheLeuProLeuAsnThrProValGluLysIleGluArgSer

3190                    3210                    3230  
AGGAGAAAGTGGCAGGCCATTGGTATCGACGCCGAGAATGGTGGCCCTGTATGACTAC  
ArgArgSerGlyArgArgHisSerValSerThrArgArgMetValAlaLeuTyrAspTyr

3250                    3270                    3290  
GACCCCAGAGAAAGCTGCCAACGTCGATGTCGAGGCCGAACTTACATTTGCACAGGA  
AspProArgGluSerSerProAsnValAspValGluAlaGluLeuThrPheCysThrGly

3310                    3330                    3350  
GATATTATTACAGTTTGGTGAATTGATGAAGATGGATTATTATGGGGAGCTGAAC  
AspIleIleThrValPheGlyGluIleAspGluAspGlyPheTyrTyrGlyGluLeuAsn

3370                    3390                    3410  
GGGCAGAAAGGCCATTGTGCCCTCAAACCTTGGAAAGAAGTGCCTGATGACGTAGAAC  
GlyGlnLysGlyLeuValProSerAsnPheLeuGluValProAspAspValGluVal

3430                    3450                    3470  
TATCTTCTGATGCTCCATCCCACTACTCTCAAGATACGCCAATGCGCTCAAAGGAAAAA

FIG. 27 F

TyrLeuSerAspAlaProSerHisTyrSerGlnAspThrProMetArgSerLysAlaLys

3490

3510

3530

AGGAAGAAGAGTGTTCATTCATACCTTAATCAGGCAATGTAGCCTCACGTAAGTGAGC  
ArgLysLysSerValHisPheIleProEnd

3550

3570

3590

AACTGAAGATAACCGATAAAAGATAACCAACTAACCTAACCGGGCCAGTGTGGTAGA

3610

3630

3650

CTTAAGGCTTCATTGTGGGGTTAAAAAAAAAAAAGATAAAAGAAATATGTCTAAAAA

3670

3690

3710

ACTATTGGACCTAAATAATTAGAATATTACTTGGTCTCAGTTGTAAGCAACTGAATTAA

3730

3750

3770

TAGTGAAGCAAATCATCTTAATAATCATTCTACTATTCATTAAGAATATTTGAAA

3790

3810

3830

GGCCAACATTGGAACATATTCCTAACAAAGCTAACGTTACATAGAGAGAGCTG

3850

3870

3890

CATATTGCATTGTTAGCCACTCTTGGAAAAGCACAACCTAACAAACATGTTACTATAG

3910

3930

3950

GAAGCTTACTTAGAAACTAACCCAAGGTCAAGCAGATGAGTAGTGAACACAGGTGAT

3970

3990

4010

CGAGTGTGGCTCTGAACACTCCAAACACTGGCTCGAGTGGCCAGAACGTGTTCTTA

4030

4050

4070

AGTAACCTGCCTCTACCTTACGAGAGAGCTATGCTCCTCTCAAAGCACAATCATCCTG

4090

4110

4130

TGACAGAAGTTGCTGCAACACGCGTTGTTGGTATACCAATGCAACTAAGTTGAT

FIG. 27 G

4150 4170 4190  
GAAGCACGCAGCTCAAATGATCACATTAGATGGAATAGATGGTATCTCAGGTGTACTTT

4210 4230 4250  
GGGATGCTTACTAGGTGTTCCATTAGAATTAGACCTTGATTTAAATCCAAGCAAGC

4270 4290 4310  
TTGAAGCCCCCTGGCTTACAGCATTGCCTGCTGAATACTAACACTCACATGGCAAGAG

4330 4350 4370  
TTGCTCTGGAGAGGTAGGCCAGAGGAATGCTGCTGCAGCGTATTAGAGTAAAAGTCTACCCC

4390 4410 4430  
AGCTGTAAAGGGAAGCGAGGTGAAGTCGTCTGCAGCGTATTAGAGTAAAAGTCTACCCC

4450 4470 4490  
TCTGAAGCACTATTAAGCGCTAACGTATATTAAATACTACCATGTGCTATCTACTGAG

4510 4530 4550  
GAAGATTCAATTGGAAATAATGCAAGCATCCACTAAGGCCTTAAGCTT

4570 4590 4610  
TCTTGATTATAATTAGGTTCAATTAGTTAGTTTTTTTTCAACCAGTGTGCCAT

4630 4650 4670  
CTCCAATATTCTATAGTATACCAACCACCCAGGAATGCACTTAACAAATATCAGGATT

4690 4710 4730  
TTATATAACCAAATAGTTCAAATACAACAAATTCCCTTATGAACCTCGCTTTAA

4750 4770 4790  
GACTACTGATGGTACTCGGCCAACCTTACTATCAACCTAACAGATCATGTCTCCCC

FIG. 27 H

4810 4830 4850  
TGCCCTTAGTCTTCATTTATGAAGTGAATTATTACCTGCCTTAGCTTGCCAAAGCAACG

4870 4890 4910  
GCCACCCCCGCACTCCCTCGAGACAGAGAAACGGAACCCACACATTTATGTCTGGGCCTC

4930 4950 4970  
TCTCTGGCGTGCTGTGGGAGAGGACCTTGCTTCTCATGGCATACTTCAACAACGTGAAAG

4990 5010 5030  
AACAAATGAACCCCCCTGACCTTCCTGGTGGAAACGGGACAGTACGATGTTACCAAG

5050 5070 5090  
TGAATTCTGTTGGCGCTCACACACTCAATAAACTGTAACACTGTACCTACTAGGTT

5110 5130 5150  
CTCCTGAGGGTTCAGGTACAGCAAGGAGAGCTCCATCCCCACAGTCCATCTCCATTGG

5170 5190 5210  
GGTCACCTACGTCATCTATGGTTCTGGTAGTCCTGGAGAGGCAGGGAAATGTCCTCGA

5230 5250 5270  
AAAAGAAAAAGGGCTGCTTCAAAGGCAAGAAACTGCTGAAAAAGCTGGTGCAGTGA

5290 5310 5330  
AATGATTCATGTGCTCCGGACAACTGCCAAATCTATGTAATTTCTTAATTCCAAACT

5350 5370 5390  
AGGGCTTCATGACTCAAGTACTCCTAAAAAAACCAATCTCTCCCTGACACCAGTA

5410 5430 5450  
GAGAAATGCACTTGCACCAACCAACTTAAACCAACCACGAGAACAAAGAGGGAGCG

5470 5490 5510

GTTGCTCTGTCACCGCTGGCAGTCTGCTCTATTGTCCAAGCTCTGATTTGGGAGGTG

5530 5550 5570  
GGAGGGGACGTCTTATTAACAAACGGGGGCAGCATAGCTATCACCTGTAGCTCCCTCCCTA

5590 5610 5630  
CCTGTAATTCCAGTCTTGTGCATTTGCATCTGCCCTAAAGGAATGATTTCAACCTT

5650 5670 5690  
TCTCCCTCTCAAAATGCTTGCCTCATAATGCATAACTTCACTTGACTCTGGTCTTGA

5710 5730 5750  
AATTCTAGTTAACCGCCTTGATGTTCTGCCTTATAAAATGCACAATGATTGTACTGT

5770 5790 5810  
CTAATAAAACAGTGTATACTTGTATGTGTCGTGCATTCACTGGTCTTCATCCTGACAC

5830 5850 5870  
AGTGGTCGAGATCAAGTTGTACAGGCTGTGCATTTAAGATACTAGTTCACTGGTCTTCAGTCTTCA

5890 5910 5930  
AAGCCAGCCAGGCTACACACAGAAAATGTTACTCAATCATTCAAAAAAGAGAAAAGGAG

5950 5970 5990  
AGAAAGTAACCTTGTGTTGGTAAAGCACCACTACTCCAACCTCCAGAAAGCCGATTATCT

6010 6030 6050  
TCATTGCTTTAATGTTCTATTCTGTGGCATATGGTTCTGTTACTTCGTTGTCAAAA

6070 6090 6110  
TGCCATACCCAAATACACAGCAATGAATGGCACACAAGTAATCCACACATAATGCATAAGCC

6130 6150 6170  
ACACCAAAACCAGACTCAATTAAATCTGCTCCAAATGAGTCCATACCCATCTTCATCAT

6190

6210

6230

TGGCATTGAACAAAAGACTTACCTACAAAGTTGCTGGCAGATGTATTGATGGTTACTC

6250

6270

6290

TTTGTAATTCTTGTCCACTTGTAAATTGTTTTACTCTTATAACATACTTTCAGACTG

6310

6330

6350

CCTTCTTTGTAATTATGGACGGTTATAAATGAATGACAAAGCTTCCCCATTGTGT

6370

6390

6410

CTTCAAAACGCTATTATAAATTGTAATATAATAGTATGTGGTAGATTATTAAAGG

6430

6450

6470

AAATCCATGTGTGGTTAACGCTCTGTGTGGGTGTGCATGTGCACAGTTAGTGTAAAATA

6490

TTTCTAGAAATAAAATTGTTATTTAT

FIG. 27 K

10	30	50
GGTCCCCACGCCAGGATGGATGAGGCCTGGGAGCAGAACGCCTGTGCACCTGGCCCTGTGC MetAspGluAlaTrpGluGlnLysProValHisLeuAlaLeuCys		
70	90	110
ATGGGCACATGCTGGAGCCGCCGTGGGCCCGCATCCTGCC <u>ACAGCCACAGGGCACCCC</u> MetGlyThrCysTrpSerArgProTrpAlaProHisPro <u>AlaThrGlyHisPro</u>		
130	150	170
GGTGTCCACCACCGTCGCCAAGGCCATGGCCCGGGAGGCCGCGCAGAGGGTGGCGAGAGC GlyValHisHisArgArgGlnGlyHisGlyProGlyGlyArgAlaGluGlyGlyGluSer		
190	210	230
AGCAGGTTAGAGAAAAGGAGCGTCTCCTAGAGAGAAAGCAGCGCGGGCAGTACGCCGCC SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla		
250	270	290
TCAGACGAGGAGGACGCCATGACTCTCCAGACTCAAGAGGAGGGCGCCTCGGTGGAC SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp		
310	330	350
GACTTCCTGAAAGGCTCTGAACCTGGCAAGCAGGAAACTGAGGCCACAGAATTGAGAA AspPheLeuLysGlySerGluLeuGlyLysGlnGlyAsnEnd		
370	390	410
TTTTGTCCATGATTACGCAGATGGTCTCCTAACAGAGCTGGAATTAGATTGAACCGAGG		
430	450	470
CCTGAAGAACGACTGTTCCACGCCCTTCCCCATGTGCCACGTTCTCCTCACCTATCCAG		
490	510	530
GAGTGAATCATCACCTCCCTGCAATCTGCTCAGGTTACAAACCCGGAGGAAAGGCTGGA		
550	570	590
GCACTTGTCTCTGGGTGAAGGACCCATAACCCCCACTGGTTTGAGATCGGCATTCAAGC		

FIG. 28 A

610                    630                    650  
GCTGTCTTATGGCAGCCMCAGCCCCAGGTGGCCCCAGAGGCCCTGACATGTGCCACCTG

670                    690                    710  
GGGCTGAGTGTGACTGAGGCCCTGAATTCTACTTCTATAAAATTAGTTCCAGATTAGTT

730                    750                    770  
TACATTCTAATTAGTTACATGTAAACAGCCACACGTGGCTGGTGGCCACCAGTGCTGA

790                    810                    830  
CGCCCAGCTCTGGATGACCACACCTGCTACAAGAGATGACTTTCTAGAGAAGAGTAGAA

850                    870                    890  
ACACAGCGGCAGAACACACAGCTCTGCACCTCCGAGGGCCTCCACTCCTCTGATGAGAC

910                    930                    950  
TGCAGAGGAAGTCTGTTGCCAAGCATGCTATTACACGTTTCCTGCTGTTTGT

970                    990                    1010  
TTAACAGAGCAAACAGGTCTGTTCTATTAAAATTAAAAAGCGTTAATATTARCAGC

1030                  1050                  1070  
ATTGTTTATGTTGTATTCTAACATAATAATAACATATTAAATTGTTAATATATA

1090                  1110                  1130  
TTGTTAATAATATAATAATATAACATAAAATAAGTGATACTTATTCCATTACAGTG

1150                  1170                  1190  
AGATATTCTTAAAAGTAACGTTAAATATTGATTCAATTCAAAGAATACATTCAATTAA

1210                  1230                  1250  
TCATACAGATGGCGTCTGGCTAGGTGACGCATCATGACAGTGGTAGGGAGTGACTGAAGT

1270                  1290                  1310

FIG. 28 B

TGAGCTGGTGCACAGACTGCCAGTTTACAACCCGGGAAGTGTTCCTGACCATCCGCTT

1330

1350

1370

CCCCATGCTGCCGCCCGTCACATGAGCCCTAACCCCTGGCGCTATCCCATCTGCTCC

1390

1410

1430

AAGACACCGATGTTCTAGTGGGTGGAAGCCTCCACTTTAGTTGACTACGGTATCTCTAG

1450

1470

1490

CATTCACACATAGTAGGTGCTCAATGAATGTTGTCGAATGAATGAAAGAAGGGA

1510

1530

1550

GGCTGAGAGTAGCTGGGACATTGCTCTGAAAAAATCACCTCCATTCTCCAAATTACA

1570

1590

1610

AAAGCATTTCATTAAGTCCACAATGAAAAAATGCTCACTGTACCAATAATAATCTTT

1630

1650

AGTTATCTATTTAAAAGTAAAAAAACCTCGTGCGAAGTC

FIG. 28 C